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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	T29839 EST97164	BX118951 BX118951	CB528492 UI-H-FT2-	CD370363 UI-H-FT1-
ID	T29839	BX118951	CB528492	CD370363
D8	14	13	4	14
Length	248	474	630	645
% Query Match	100.0	100.0	100.0	100.0
Score	43		43	
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ALIGNMENTS

Homo sapiens (human)

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 248)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A.,

Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald

L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., HinkleJr, P.S., Kelley, J.M.,

Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J.,

Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W.,

Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L.,

Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei EST97164 Human Testis Homo sapiens cDNA 5' end similar to tumor necrosis factor, alpha (HT:1190), mRNA sequence.
T29839.1 GI:611937 DEFINITION ORGANISM REFERENCE AUTHORS ACCESSION KEYWORDS RESULT 1 T29839 VERSION

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Similarity
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SOURCE
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                                                             Patterns
                                                                                                                                                Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
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Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston

Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 474)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.

Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3

Unpublished

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPDIS INAGP9981124300.

RZPDIS INAGP9981124300.

RZPDIS INAGP981124300.

RZPDIS INAGP9981124300.

RZPDIS INAGP981124300.

RZPDIS INAGP9981124300.

RZPDIS INAGPS CloneCards/cgi-

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seg prime

This clone is sequence: TTCACACACAGGAAACAGCTATGAC.

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BX118951
BX118951 Soares fetal heart NDHH19W Homo sapiens cDNA clone IMAGP998L124300; IMAGE:1693595, mRNA sequence.
BX118951
BX118951.1 GI:27882696
                                                          Diversity and Expression of cDNA Sequence
,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone_lib="Human Testis"
/note="Organ: testis"
a 65 c 60 g 57 t
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Pred. No. 8.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
       Lutial Assessment of Human Gene Di Based Upon 83 Million Basepairs of Nature 377, 3-174 (1995) 96026280 7566098
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source

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UI-H-FT2-bjd-e-20-0-UI.81 NCI CGAP FT2 Homo sapiens cDNA clone UI-H-FT2-bjd-e-20-0-UI 3', mRNA sequence. CB528492 CB528492.1 GI:29388228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 1-29, >AT rich#Low complexity (matched compliment)

205-279, > (TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjd-e-20-0-UI"
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/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 630)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 43; DB 13;
100.0%; Pred. No: 0.00011;
ive 0; Mismatches 0;
'mol_type="mRNA"
'db_xref="taxon:9606"
'clone="IMAGp998L124300
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Page

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/ Organism="Homo sapiens"
// organism="Homo sapiens"
// organism="Homo sapiens"
// db_xref="taxon:9606"
// clone="UI-H-FT1-bkb-n-03-0-UI"
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// lab_host="DH10B (Life Technologies)"
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// note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
// NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.
// Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag
                              ed from
                                                                                                                 Genome
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                                                                                                                                         by Dr.
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genor Research, 6:791-806, 1996. The tissue was provided by Dr Gary W. Hunninghake of the University of Iowa.

TAG LIB=UI-H-FT2

TAG TISSUE=Human Lung Aveolar Macrophage

TAG SEQ=GGCCATGCCG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Iow

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iow

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 294-368, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 645)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (Compublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        645 bp mRNA linear EST 2
UI-H-FT1-bkb-n-03-0-UI.81 NCI CGAP FT1 Homo sapiens CDNA
CD370363
CD370363.1 GI:31154452
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                                                                                                                                                                                                                                                                                                                                                                         630;
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Pred. No. 0.00011;
Mismatches 0;
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DEFINITION

Matches

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BASE CO

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

ACCESSION VERSION KEYWORDS SOURCE

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1. .684

/ organism="Homo sapiens"
// organism="Homo sapiens"
// organism="UI-H-FT1-bic-i-01-0-UI"
// tissue type="Aveolar Macrophage"
// dev stage="Adult"

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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 297-371, > (TAAA)n#Simple_repeat

Seq primer: M13 FORWARD
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 684)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG LIB=UI-H-FT1

TAG LIB=UI-H-FT1

TAG SEQ=GGCCATGCCG"

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CA307429
CA307429.1 GI:24470483
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjr-l-14-0-UI"
/tisue type="Aveolar Macrophage"
/dev_stage="Aveolar Macrophage"
/dev_stage="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone lib="NCI CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Site_1: Site_2: Not I;
NCI CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EccR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of lowa.

TAG_LIB=UT-H-FT1
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CD367676
EST 29-MAY-CD367676
CD367676.1 GI:31151766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Ic

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Ic

DNA Sequencing by: Dr. M. Bento Soares, University of Icwa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 69-143, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 688)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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Pred. No. 0.00012;
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TAG_LIB=UI-H-FT1
TAG_TISSUE=Human Lung
TAG_SEQ=GGCCATGCCG"
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A linear EST 01-NOV-2002 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtaine

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 296-370, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 696)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished
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                                                        Length 688;
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TAG_SEQ=GGCCATGCCG"
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UI-H-FT1-bhu-n-04-0-UI 3',
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Homo sapiens
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Lorganism="Momo sapiens"

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UI-H-FTI-bhy-e-14-0-UI.sl NCI_CGAP_FT1 Homo sapiens cDNA clone
             CD368142

UI-H-FT1-bjv-e-20-0-UI.81 NCI_CGAP_FT1 Homo sapiens cDNA clone
UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.
CD368142

CD368142.1 GI:31152232
                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 298-372, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD
                                                                                                                                                                                                   Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 703)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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larity 100.0%; Pred. No. 0.00012;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 699)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Ic

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Ic

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 296-370, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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CD364761.1 GI:31148851
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Pred. No. 0.00012;
Mismatches 0;
                        Score 43; DB 14;
Pred. No. 0.00012;
Mismatches 0;
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                        th 100.0%; Similarity 100.0%; 43; Conservative
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Homo sapiens (human) Homo sapiens

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

ACCESSION VERSION KEYWORDS SOURCE

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Location/Qualifiers

Location/Qualifiers

1. 719

/ organism="Homo sapiens"

/ mol type="mRNA"

/ db xref="taxon:9606"

/ clone="UI-H-FT2-bjd-1-22-0-UI"

/ tissue_type="Avoclar Macrophage"

/ dev stage="Adult"

/ lab_host="DH10B (Life Technologies)"

/ lab_host="Macrophage"

/ note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;

NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996; The tissue was provided by Dr.

Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Aveolar Macrophage

TAG_TISSUE=Human Lung Aveolar Macrophage

TAG_SEQ=GGCCATGCCG"

163 g 188 t 2 others
                                                         Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.

I (bases 1 to 719)

NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA sequence: 294-368, > (TAAA) n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
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1. (bases 1 to 722)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished
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UI-H-EII-azb-j-22-0-UI.s1 NCI CGAP EII Homo sapiens
IMAGE:5846517 3', mRNA sequence.
BQ007008
BQ007008.1 GI:19731908
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100.0%; Pred. No. 0.00012;
ive 0; Mismatches 0;
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Location/Qualifiers

Location/Qualifiers

/ organism="Homo sapiens"
/ mol_type="mRNA"
/ db_xref="taxon:9606"
/ clone="UI-H-FTI-bhy-e-14-0-UI"
/ tissue_type="Adult"
/ lab_host="DH10B (Life Technologies)"
/ clone lib="NCI_CGAP_FTI"
/ lab_host="DH10B (Life Technologies)"
/ clone lib="NCI_CGAP_FTI"
/ lote="Torgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCG. The tissue was provided by Dr. Gary W.
Handinghake of the University of Iowa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iowa
                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares University of Iowa Clone Distribution: Clone distribution information can be obtaine from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA sequence: 296-370, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Unpublished
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UI-H-FT2-bjd-l-22-0-UI.S1 NCI CGAP FT2 Ho UI-H-FT2-bjd-l-22-0-UI 3', mRNA sequence CB528694
CB528694.1 GI:29388630
UI-H-FT1-bhy-e-14-0-UI 3', mRNA sequence.
CA308256
CA308256.1 GI:24471310
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Location/Qualifiers

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TAG_LIB=UI-H-FT1
TAG_TISSUE=Human Lunc
TAG_SEQ=GGCCATGCCG"
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Query Match Best Local S Matches 43

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RESULT 11 CB528694/c LOCUS

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// Organism="Homo sapiens"
// Ab _ xref="taxon:9606"
// Ab _ xref="taxon:9606"
// Clone="IMAGE:5846517"
// tissue_type="Chondrosarcoma"
// dev stage="Adult"
// lab_host="DH10B (Life Technologies)"
// clone=lib="NCI CGAP EII"
// lab_host="DH10B (Life Technologies)"
// clone=lib="NCI CGAP EII"
// lab_host="DH10B (Life Technologies)"
// lab_host="DH10B (Life Technologies)"
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// lab_host="DH10B (Life Technologies)"
// clone=lib="NCI CGAP EII"
// lab_host="DH10B (Life Technologies)"
// lab_host="Driane (SAP EII"
// lab_host="Dharmacia"
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// lab_host="Dharmacia"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of
cDNA Library Arrayed by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be f
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl
The following repetitive elements were found in this cDNA
sequence: 297-371, > (TAAA) n#Simple_repeat
Seq primer: M13 FORWARD
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of

CDNA Library Arrayed by: Dr. M. Bento Soares, University of

DNA Sequencing by: Dr. M. Bento Soares, University of
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (Tumor Gene Index
Unpublished
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UI-H-FT1-bhu-o-04-0-UI.81 NCI CGAP FT1 Homo sapiens
UI-H-FT1-bhu-o-04-0-UI 3', mRNA sequence.
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Pred. No. 0.00012;
); Mismatches 0;
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TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTGCAC"
162 c 164 g 190
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larity 100.0%;
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CA307062/c
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RAUTHORS

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/tissue_type="Aveolar Macrophage"
/dev atage="Adult"
/lab_host="Mault"
/lab_host="Mault"
/clone lib="NCI_CGAP_FTI"
/clone lib="NCI_CGAP_FTI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCG. The tissue was provided by Dr. Gary W. Hunninghase of the University of Iowa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9-MAY-2003
clone
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 722)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of

cDNA Library Arrayed by: Dr. M. Bento Soares, University of

cDNA Library Arrayed by: Dr. M. Bento Soares, University of

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found a

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 295-369, > (TAAA) n#Simple_repeat
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 2
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Sapiens
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TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 14;
Pred. No. 0.00012;
0; Mismatches 0;
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UI-H-FT2-bjn-c-04-0-UI.81 NCI CGAP FT2 Hc
CD364988
CD364988.1 GI:31149078
                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-o-04-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 723)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Ic

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Ic

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Ic

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Ic

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Ic

cDNA Sequencing by: Cone distribution information can be obta

from Dr. M. Bento Soares, bento-soares@wiowa.edu

The following repetitive elements were found in this cDNA

sequence: 297-371, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yee.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-b-23-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 14;
Pred. No. 0.00012;
Mismatches 0;
           repeat
        > (TAAA) n#Simple_
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                                                    Location/Qualifiers
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Seq primer: M13 FORWARD POLYA=Yes.
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Homo sapiens
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Matches 43
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CA308777/c
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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COMMENT

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/clone lib="NCI CGAF Fix / note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; Note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with I; Note="Organ: Lung; Vector I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag synthesis of first-strand cDNA contains a library tag
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                                                                                                                                                                                                                                                                                                                                                                                                             sequence that is located between the Not I site (dT)18 tail. The sequence tag for this library GGCCATGCCG. The tissue was provided by Dr. Gary Hunninghake of the University of Iowa.
TAG LIB=UI-H-FT1
TAG LIB=Human Lung Aveolar Macrophage
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Pred. No. 0.00012;
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llarity 100.0%;
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5.1.6
Compugen Ltd
version
- 2004
GenCore
(c) 1993
        Copyright
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Bec. ; Search time 764.932 Second (without alignments) 207.072 Million cell updates. 05:14:03 sw model using 2004, nucleic search, m February OM nucleic Run

US-09-801-371A-2 Title: Perfect

, actggggcctacagctttga tcaaactggggcctccagaa score: Sequence:

43

Scoring table:

0. Gapext IDENTITY NUC Gapop 10.0 , residues 1841816367 2449703 seqs, Searched:

4899406 hits satisfying chosen parameters: ğ Total number

2000000000 length: length: 86 Q 08 08 08 Minimum Maximum

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

Published Database

cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

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cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:* 406456786441144141040645678

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. No. score grea and is der

SUMMARIES

	ript	equence 2, A	Sequence 6, Appli	Sequence 8, Appli	Sequence 7, Appli.	1, Appl	5,	120, A	equence 9, Appl	4	m	Sequence 4, Appli	68, Ap	1, App	34,	104, A
	Q	US-09-801-371A-2	US-09-801-371A-6	US-09-801-371A-8	US-09-801-371A-7	US-09-801-371A-1	US-09-801-371A-5	US-10-247-671-120	US-10-310-793-9	US-10-272-411-4	US-10-218-547-3	US-10-272-328A-4	US-10-247-671-68	US-09-824-322B-1	US-09-932-300-34	US-10-191-997-104
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equence 33, Ap	quence 24, App	equence 6223, A	ence 6223, A	equence 6223, A	quence 6223, A	equence 10, App	equence 2, App	equence 1127, A	e 110108,	equence 110108	equence 46829	1069	quence 11069	equence 12008	quence 120081	equence 11, Ap	equence 1, App	equence 1056	e 146, Ap	equence 279282,	e 279282,	equence 36947,	equence 72, App	equence 72, App	equence 1	equence 126, Ap	equence 779, Ap	80, A	equence 12, App
-10-429-802-3	-10-430-503-2	-09-796-692-622	-10-057-475B-622	-10-154-884B-6	-10-040-862-622	-801-371A-1	5-10-312-84	-09-535-459-112	-10-027-632-11010	-10-027-632-11010	-10-242-535A-4682	-10-027-632-11069	-027-632-1	-10-027-632-12008	-10-027-632-12008	-09-801-371A-11	S-10-312-841-1	09-783-590-10	-09-560-863-14	-10-027-632-2792	-10-027-632-27928	-10-369-493-3694	-09-981-876-7	-09-148-545-7	-09-981-876-12	-09-148-545-12	-09-925-300-7	-09-764-891-55	-252-157-1
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ALIGNMENTS

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APPLICANT: Kaempfer, Raymond
APPLICANT: Kaempfer, Raymond
APPLICANT: Osman, Farhat
APPLICANT: Jarrous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
ITTLE OF INVENTION: REGULATION OF MRNA SPLICING AND ITS USES
TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR PILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 43;
Sequence 2, Application US/09801371A Patent No. US20020155569A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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; LENGTH: 43
; TYPE: DNA
; ORGANISM: Hom
US-09-801-371A-2
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SEQ ID NO 2
LENGTH: 4
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Indels ö Score 43; DB 10; Pred. No. 5.6e-08 Mismatches 0 . 0 100.0%; Conservative Query Match Best Local Similarity Matches 43; Conser ठ

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Application US/09801371A JS20020155569A1 RESULT 2 US-09-801-371A-6/c Sequence Patent No GENERAL I

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Sequence 8, Application US/09801371A

Patent No. US20020155569A1

GENERAL INFORMATION:

APPLICANT: Kaempfer, Raymond

APPLICANT: Osman, Farhat

APPLICANT: Jarrous, Nayef

APPLICANT: Ben-Asouli, Yitzhak

TITLE OF INVENTION: REQULATION OF GENE EXPRESSION THROUGH

TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USE

FILE REFERENCE: A34084-PCT-USA-A 066031.0147

CURRENT APPLICATION NUMBER: US/09/801,371A

CURRENT APPLICATION NUMBER: PCT WO 00/14255

PRIOR FILING DATE: 1999-09-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                           Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 50;
APPLICANT: Osman, Farhat
APPLICANT: Osman, Farhat
APPLICANT: Jarrous, Nayef
APPLICANT: Jarrous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS US
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 7, Application US/09801371A

Patent No. US20020155569A1

GENERAL INFORMATION:

APPLICANT: Kaempfer, Raymond

APPLICANT: Osman, Farhat

APPLICANT: Jarrous, Nayef

APPLICANT: Ben-Asouli, Yitzhak

TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH

TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS

FILE REFERENCE: A34084-PCT-USA-A 066031.0147
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Pred. No. 5.6e-08;
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; Sequence 5, Application US/09801371A
; Patent No. USZ0020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MENA SPLICING AND ITS USF
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 1999-09-06
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
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Sequence 1, Application US/09801371A

Patent No. US20020155569A1

GENERAL INFORMATION:

APPLICANT: Kaempfer, Raymond

APPLICANT: Osman, Farhat

APPLICANT: Osman, Farhat

APPLICANT: Jarrous, Nayef

APPLICANT: Ben-Asouli, Xitzhak

TITLE OF INVENTION: MANIPULATION OF MENE SPLICING AND ITS

FILE REFERENCE: A34084-PCT-USA-A 066031.0147

CURRENT APPLICATION NUMBER: US/09/801,371A

CURRENT APPLICATION NUMBER: PCT WO 00/14255

PRIOR APPLICATION NUMBER: PCT WO 00/14255

PRIOR FILING DATE: 1999-09-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 104

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Pred. No. 5.6e-08;
Mismatches 0
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Pred. No. 5.6e-08;
; Mismatches 0
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 81
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Similarity 100.0%;
43; Conservative 0
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Similarity 79.1%;
34; Conservative 9
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US-09-801-371A-7
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Pred. No. 5.7e-08;
Mismatches 0:
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Pred. No. 5.7e-08;
0; Mismatches 0;
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ X01394.1
DATABASE ENTRY DATE: 1995-03-21
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-05-01
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
DATABASE ENTRY DATE: 2002-08-01
RELEVANT RESIDUES: (1)..(1643)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES TH
FILE REFERENCE: 60019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43;
Pred. No.
                                                                                                                                                                                                                                  removed
PRIOR FILING L. 2000-07-07

PRIOR APPLICATION NUMBER: 09/559,290

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/180,908

PRIOR FILING DATE: 2000-02-08

PRIOR FILING DATE: 1999-05-13

PRIOR FILING DATE: 1999-05-13

PRIOR FILING DATE: 1999-05-03

REMAINING PATE: 1999-05-03

Remaining Prior Application data removing NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 1643
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Publication No. US20030100068A1
GENERAL INFORMATION:
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larity 100.0%;
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; ORGANISM: human
US-10-310-793-9
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TYPE: DNA
ORGANISM:
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US-10-310-793-9
Sequence 9, Application US/10310793
Publication No. US20030198640A1
Publication No. US20030198640A1
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Wel, Ping
TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory B
TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
FILE REFERENCE: PP573
CURRENT APPLICATION NUMBER: US/10/310,793
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: 60/336,695
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 60/314,381
PRIOR PILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/278,449
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                                                                                                          Length 104
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OTHER INFORMATION: Incyte ID No. US20030194721A1 561301CB1
10-247-671-120
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                                                                                                                                                                                                                                                                                RESULT 7
US-10-247-671-120
; Sequence 120, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Raser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOA
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL PROGram
; SEQ ID NO 120
; LENGTH: 1279
                                                                                                          Score 43; DB 10;
Pred. No. 5.6e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 13;
Pred. No. 5.7e-08;
Mismatches 0;
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Best Local Similarity 100.0%;
Matches 43; Conservative (
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Best Local Similarity 100.0%;
Matches 43; Conservative
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                                                 sapien
                                                 Homo
         ; LENGTH: 104
; TYPE: DNA
; ORGANISM: Hom
US-09-801-371A-5
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Sequence 1, Application US/09824322B;
Publication No. US20030022848A1
GENERAL INFORMATION:
APPLICANT: Baker, Brenda
APPLICANT: Bather, C. Frank
APPLICANT: Butler, Madeline M.
APPLICATION NUMBER: US/09/824,322B
CURRENT FILING DATE: 1999-05-18
PRIOR PILING DATE: 1999-05-18
PRIOR PILING DATE: 1998-10-05
NUMBER OF EQ ID NO 1
SEQ ID NO 1
LENGTH: 3634
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Pred. No. 5.7e-08;
Mismatches 0;
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(796..981,1589..1634,1822..1869,2171
APPLICANT: Mikita, Thomas
APPLICANT: Shiffman, Dov
APPLICANT: Shiffman, Dov
APPLICANT: Porter, Gordon, J.
APPLICANT: Raser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREAT
FILE REFERENCE: PA-0050 US
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL Program
SEQ ID NO 68
LENGTH: 1666
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NOFER INFORMATION: INCOME INFORMATION: Incyte ID NOFER INFORMATION: Incyte ID NOFER INFORMATION: INCOME INFOR
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ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: 1347, 1358
; OTHER INFORMATION: a,
US-10-247-671-68
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Best Local Similarity
Matches 43; Conser
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Sequence 3, Application US/10218547

Publication No. US20030100074A1

GENERAL INFORMATION:
TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bond TITLE OF INVENTION: Human Endokine Alpha

FILE REFERENCE: PF561

CURRENT APPLICATION NUMBER: US/10/218,547

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: 60/312,542

PRIOR FILING DATE: 2001-08-16

PRIOR FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin version 3.1
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                                                                               TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
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APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Lam, Jonathan
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF; FILE REFERENCE: 60019620-0206; CURRENT FILING DATE: 2003-01-24; PRIOR FILING DATE: 2001-10-15; NUMBER OF SEQ ID NOS: 51
SEQ ID NO 4
SEQ ID NO 4
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Pred. No. 5.7e-08;
Mismatches 0;
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Pred. No. 5.7e-08;
Mismatches 0
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US-10-247-671-68
; Sequence 68, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
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ID NO 3
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TYPE: DNA
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US-10-272-328A-4
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US-10-218-547-3
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; Sequence 34, Application US/09932300
; Publication No. US20030032788A1
; GENERAL INFORMATION:
; APPLICANT: GARVER, Eric
; APPLICANT: TU, Guang-Chou
; APPLICANT: ISRAEL, Yedy
; TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION
; FILE REFERENCE: 9855-3U2
; CURRENT FILING DATE: 2001-08-20
; CURRENT FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/051,705
; PRIOR APPLICATION NUMBER: US 09/109,663
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patentin Ver. 2.1
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Publication No. US20030207834A1
GENERAL INFORMATION:
APPLICANT: Oligos Etc., Inc.
APPLICANT: DALE, Roderic M. K.
APPLICANT: ARROW, Amy
APPLICANT: THOMPSON, Terry
TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological
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LOCATION: (2171)...(3381)

PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Smith, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor gentitle: chromosomal localization
JOURNAL: Nucleic Acids Res.
VOLUME: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 11;
Pred. No. 5.8e-08;
; Mismatches 0;
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Pred. No. 5.8e-08;
; Mismatches 0;
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PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE ENTRY DATE: 1997-02-17
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US-10-191-997-104
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LENGTH: 3634
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US-09-932-300-34
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US-09-824-322B-1
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| FILE REFERENCE: 54800-5019
| CURRENT APPLICATION NUMBER: US/10/191,997
| CURRENT FILING DATE: 2002-07-10
| PRIOR APPLICATION NUMBER: US 60/303,820
| PRIOR FILING DATE: 2001-07-10
| NUMBER OF SEQ ID NOS: 132
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 104
| LENGTH: 3634
| TYPE: DNA
| ORGANISM: Homo sapiens
| ORGANISM:
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Sequence Sequence

US-09-313-932-212 US-09-313-932-213 US-09-313-932-214 US-09-313-932-354 US-09-313-932-357 US-09-313-932-358 US-09-313-932-361 US-09-632-098-1 US-09-632-098-1 US-08-231-193A-57 US-08-940-086A-57 US-08-940-035A-57 US-08-935-105A-57 US-09-935-105A-57 US-09-935-105A-57 US-09-935-105A-57 US-09-935-105A-57

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'cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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US-09-166-186-1

US-09-166-186-1

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US-09-109-663-34

US-09-109-663-34

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US-09-109-63-34-1

US-08-470-298B-1

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US-09-361-737-1

US-09-361-737-1

US-09-361-737-1

US-09-734-036-1

US-09-784-316-3

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Therapy Corporation Box 368 벙 d Apoptosis of Cells by Gene region UNMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: Boehringer Ingelheim Corpostreet: 900 Ridgebury Road, P.O. Box CITY: Ridgefield STREET: 900 Ridgebury Road, P.O. Box CITY: Ridgefield STATE: Connecticut COUNTRY: United States of America ZIP: 06877-0368
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,297A
FILING DATE: 27-Feb-1998
CLASSIFICATION NUMBER: 60/038,266
FILING DATE: 28-FEB-97
ATTORNEY/AGENT INFORMATION:
NAME: Robert P. Raymond
REGISTRATION NUMBER: 25089
REFERENCE/DOCKET NUMBER: 9/121PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-791-6183
FORMATION FOR SEQ ID NO: 13:
SEQUENCE THARACTERISTICS:
LENGTH 129 þ Steven f. Tatake, Steven
W. Barton
Self-Regulated
Inflammatory Ce untranslat Q ID NO: 1 US-09-032-297A-13
; Sequence 13, Application US/09032297A
; Patent No. 6525184
; GENERAL INFORMATION: SEQ TYPE: nucleic acid STRANDEDNESS: singl TOPOLOGY: linear 'n /KEY: TNFa DESCRIPTION: ٦. ۳. APPLICANT: Revati J. Randall W TITLE OF INVENTION: DESCRIPTION: NAME/ SEQUENCE -09-032-297A-13 FEATURE INFORMATION RESULT Appli Appli Appli Appli Appli Applitable

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09505250A; Sequence 4, Application US/09505250A; Patent No. 6329148; GENERAL INFORMATION: APPLICANT: Rosen, Glenn; APPLICANT: Kao, Peter; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy; TITLE OF INVENTION: Triptolides and Death Domain Lig; FILE REFERENCE: SUN-109PRV2; CURRENT APPLICATION NUMBER: US/09/505,250A; CURRENT FILING DATE: 2000-02-15; NUMBER OF SEQ ID NOS: 4; SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.7e-08;
Mismatches 0;
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Pred. No. 1.7e-08;
; Mismatches 0;
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APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-09-229-151C-13
Sequence 13, Application US/09229151C
Patent No. 6537784
GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
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100.0%; Pr
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                                                                                                                       TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TNF CDN
INDIVIDUAL ISOLATE: #X01394
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US-09-505-250-4
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NAME/KEY: CDS
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LENGTH: 1643
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; LOCATION:
US-08-880-342-36
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Matches 43
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US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by C
; TILE REFERENCE: 9/137
; TILE REFERENCE: 9/137
; CURRENT FILING DATE: 1999-01-12
; PRIOR PILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 2.0
; SEQ ID NO 7.
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APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
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                                                          TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.2
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                                         TCAAACTGGGGCCTCCAGAACTCACTGGGGGCCTACAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 4; 1
Pred. No. 1.5e-08;
; Mismatches 0;
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350 Cambridge Avenue, Suite 250
    Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,34
FILING DATE: 23-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSULT 3
3-08-880-342-36
Sequence 36, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
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Similarity 100.0%;
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    Conservative
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ADDRESSEE: Deblinger
STREET: 350 Cambridge
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Human FEATURE:
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US-08-8
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APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNP-
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: ISPH-0356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/313,932A CURRENT FILING DATE: 1999-05-18 NUMBER OF SEQ ID NOS: 501
     SEQ ID NOS:
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(1635).
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                                                   TYPE: DNA
ORGANISM: Homo (FEATURE:
NAME/KEY: CDS
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NAME/KEY:
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     NUMBER OF
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                                    Inflammatory
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APPLICANT: Baker, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF FILE REFERENCE: ISPH-0322
CURRENT APPLICATION NUMBER: US/09/166,186A
CURRENT FILING DATE: 1998-10-05
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Pred. No. 1.8e-08;
; Mismatches 0;
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US-09-229-151C-14

Sequence 14, Application US/09229151C

Patent No. 6537784

GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Marlin, Steven D.
APPLICANT: Barton, Randall W.
TITLE OF INVENTION: Self-Regulated Apoptosis of FILE REFERENCE: 9/137
CURRENT APPLICATION NUMBER: US/09/229,151C
CURRENT FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: US 60/076,316
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 2.0
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APPLICANT: Marlin, Steven D.
APPLICANT: Barton, Randall W.
TITLE OF INVENTION: Self-Regulated Apoptosis of
FILE REFERENCE: 9/137
CURRENT APPLICATION NUMBER: US/09/229,151C
CURRENT FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: US 60/076,316
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 2.0
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Pred. No.
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US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
                                                                                                                                                                                             TYPE: DNA
CRGANISM: Human
FEATURE:
CTHER INFORMATION: chimeric gene
US-09-229-151C-13
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FEATURE:
OTHER INFORMATION: C
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LENGTH: 2270
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Best Local S
Matches 43
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Best Local
Matches 4
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2e-08;
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Best Local Similarity 100.0%; Pred. No. 2e
Matches 43; Conservative 0; Mismatches
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DATE: 1985-09-11

DATABASE ACCESSION NUMBER: X02910 Genbank

DATABASE ENTRY DATE: 1997-02-17
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Patent No. 6228642
GENERAL INFORMATION:
APPLICANT: Baker, Brenda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL: Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: Pennica, D. AUTHORS: Goeddel, D.V. AUTHORS: Gray, P.W. TITLE: Human lymphotoxin at TITLE: homology and chromo
                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (2171)...(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Naylor, S.L.
AUTHORS: Sakaguchi, A.Y.
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Jarrett-Nedwin,
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(1870)..(2070)
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(982)..(1588)
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25; Conserv
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US-09-740-027-3
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OPERATING
SOFTWARE:
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                                                                                                                                                                                                                                                         740-027-3
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Best Local S
Matches 25
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                                                                                                           Query Match
Best Local S
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US-09-109-663-34

Sequence 34, Application US/09109663

Patent No. 6277981

GENERAL INFORMATION:

APPLICANT: Tu, Guang-Chou

APPLICANT: Israel, Yedy

TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF

TITLE OF INVENTION: BFFICACIOUS ANTISENSE OLIGONUCLEOTIDES

TITLE OF INVENTION: BFFICACIOUS ANTISENSE OLIGONUCLEOTIDES

TITLE OF INVENTION: BFFICACIOUS ANTISENSE OLIGONUCLEOTIDES

CURRENT APPLICATION NUMBER: US/09/109,663

CURRENT FILING DATE: 1998-07-03

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin Ver. 2.0
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PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor genes:
TITLE: structure, homology and chromosomal localization
JOURNAL: Nucleic Acids Res.
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Best Local Similarity 100.0%; Pred. No. 3
Matches 43; Conservative 0; Mismatch
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DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE ENTRY DATE: 1997-02-17
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(1822)..(1869)
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(1589)..(1634)
                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (796..981,158)
                                                                                                              exon (615)..(981)
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LOCATION:
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NAME/KEY:
LOCATION:
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NAME/KEY:
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NAME/KEY:
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Patent No. 646577.

GENERAL INFORMATION:
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
TITLE OF INVENTION: COPACTOR PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001052
CURRENT APPLICATION NUMBER: US/09/740,027
CURRENT APPLICATION NUMBER: US/09/740,027
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GENERAL INFORMATION:
APPLICANT: LAFEMINA, R.
APPLICANT: SARDANA, V.
APPLICANT: VELOSKI, C.
TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROY D. MEREDITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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Pred. No. 2e-08;
Mismatches
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Pred. No. 16;
0; Mismatches
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                                                 ; OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34
                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09740027
Patent No. 6485939
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ATTORNEY/AGENT INFORMATION:
NAME: MEREDITH, ROY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DY D. MERE
BOX 2000,
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TYPE: DNA ORGANISM: Homo sapiens
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us-09-801-371a-2

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TELECOMMUNICATION TELEPHONE: (908
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                                                                                                                               Sequence 5, Applicat
GENERAL INFORMATION
APPLICANT: LAFEM
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
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STREET: 94
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APPLICANT:
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APPLICANT:
APPLICANT:
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CITY: R
STATE:
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Matches 27
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PCT-US95-12987-3
; Sequence 3, Application PC/TUS9512987
; GENERAL INFORMATION:
; APPLICANT: LAFEMINA, R.
; APPLICANT: VELOSKI, C.
; TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
; TITLE OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
; TITLE OF INVENTION: 126 E. LINCOLN AVE.
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Pred. No. 13;
); Mismatches ]
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Mismatches
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Pred. No.
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ADDRESSEE: ROY D. MEREDITH
STREET: P.O. BOX 2000, 126 E. LINCO
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTON:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12987
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEREDITH, ROY D.
REGISTRATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 1926;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4678
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
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STABLE RECOMBINANT HCMV PROTEASE
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12987
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Patent No. 5658758
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ilarity 73.0%;
Conservative
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NAME: MEREDITH, ROY D.
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
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O KEY WEST AN
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Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A
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nucleic acid
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                    Floppy
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COMPUTER READABLE FORM
MEDIUM TYPE: Floppy
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VELOSKI,
                                                                                                                  RAHWAY
NEW JERSEY
                                                                  INVENTION:
                                                                                                                                                                                                                               OPERATING SYSTEM:
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27; Conserv
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ZIP: 07065-0907
COMPUTER READABLE
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US-08-470-298B-1

Sequence I. Application US/0847029BB

Patent No. 5844081

GENERAL INFORMATION:

APPLICANT: NI, JIAN

APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: CYTOSTATIN I

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: HUMAN GENOME SCIENCES, INC.

STREET: 40410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PALOMES: PC-DOS/MS-DOS

SOFTWARE: PROCKVILLE

SOFTWARE: PALOMES: US/08/470,298B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROCKES, ALLAN A.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF175D1

TELEPHONE: 301-309-8512

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 861 base pairs

TYPE: nucleic acid
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,731A
FILING DATE: 24-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF175
TELECOMMUNICATION INFORMATION:
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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AAN6 AAN6 AAF AAF AAN8 AAN6 AAN6	AAN60 AAT1 AAN71 AAT3 ABK1 AAD4	AAZ209 AAZ209 AAV390 AAX090 AAA407 AAD456 AAD456 AAF574	AAF2 AAF2 AAF2 AAA3 AAO2 AAO2 AAO2
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ALIGNMENTS

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AAZ99817 standard; RNA; 43

RESULT 1

alpha-subuni : 2; eIF2alph Cis-acting nucleotide sequence derived from human TNF-alpha intron removal rotein kinase; factor alpha; 98IL-0126112. 98IL-0126757. (YISS) YISSUM RES & DEV CO. 99WO-IL00483. (first entry) Cis-acting sequence, RNA-activated protei tumour necrosis fact WPI; 2000-257000/22 WO200014255-A1. Homo sapiens. 06-SEP-1999; 16-MAR-2000. 07-SEP-1998; 26-OCT-1998; Kaempfer R, 12-JUL-2000 AAZ99817;

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The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryot initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the splicing level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNU splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structun protein) or industrially or agriculturally applicable protein. The protein is sequence represents a cis-acting nucleotide sequence of the
Regulation of gene expression by mRNA splicing is carried out cis-acting nucleotide sequence controlled by phosphorylation alpha-subunit of eukaryotic initiation factor 2
                                                                                                                                                                              English
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                                           cis-acting nuc
alpha-subunit
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T; 0 other; 43 BP; 10 A; 13 C; 11 G; 9 Sequence

ö Length 43; Indels 43 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA CACTGGGGCCTACAGCTTTGA ö th 100.0%; Score 43; DB 21; Similarity 100.0%; Pred. No. 1.9e-07 43; Conservative 0; Mismatches 0 Query Match Best Local S Matches 43 ႕ g Š

RESULT AAZ998:

standard; RNA; AAZ99815; AAZ99815

ВР

20

(first entry) 12-JUL-2000 tumour necrosis factor-alpha gene the stem loop of ö Sequence

alpha Cis-acting sequence, intron removal, trans-acting factor, alpha-sul RNA-activated protein kinase, eukaryotic initiation factor 2, eIF2; tumour necrosis factor alpha, TNF-alpha, gene therapy, ss.

Homo sapiens

WO200014255-A1

16-MAR-2000

99WO-IL00483 06-SEP-1999;

98IL-0126112 98IL-0126757 07-SEP-1998; 26-OCT-1998;

DEV CO ß (YISS) YISSUM RES

Regulation of gene expression by mRNA splicing is carried out cis-acting nucleotide sequence controlled by phosphorylation calpha-subunit of eukaryotic initiation factor 2 -Ben-Asouli Jarrous N, Œ 2000-257000/22. Osman Kaempfer R,

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English 75pp; 5B; 7; Fig Example

įs sequence which specification describes a cis-acting nucleotide The

capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated corporation of a trans-acting the alpha-subunit of eukaryotic initiation factor 2 (eIFZalpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the splicing of practivated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a fragment of the 3'UTR of human TNF-alpha.

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0 other; ů, 11 A; 15 C; 12 G; Sequence 50 BP; 12

Gaps .. 0 Length 50 Indels 0 21; 43; br Mismatches 8 Score Pred 6 ٠., 100.0%; 79.1%; Conservative ery Match st Local Similarity Eches 34; Conserv Matches Best

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47 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA Н a ਨੇ

AAZ9981 RESULT

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Gaps

ВЪ AAZ99816 standard; RNA; 104

AAZ99816;

entry) (first 12-JUL-2000 Cis-acting nucleotide sequence derived from human TNF-alpha

Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit; RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha; tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

Homo sapiens

WO200014255-A1

16-MAR-2000

99WO-IL00483. 06-SEP-1999; 98IL-0126112. 98IL-0126757. 07-SEP-1998; 26-OCT-1998;

Ben-Asouli z Jarrous CL, Osman ц, Kaempfer

& DEV CO.

(YISS) YISSUM RES

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WPI; 2000-257000/22.

ĸ using of the Regulation of gene expression by mRNA splicing is carried out cis-acting nucleotide sequence controlled by phosphorylation alpha-subunit of eukaryotic initiation factor 2

75pp; English 15; 4; Page Claim

The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders

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This sequence represents a human TNFalpha (tumour necrosis factor alpha)

3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984)

were constructed comprising at least one TNFalpha promoter enhancer

region (AAZ20975-Z20978), a TNFalpha promoter (AAZ20972-Z20974), a DNA

encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a

TNFalpha 3'UTR sequence. TNFalpha is one of a number of

cytokines produced by inflammatory cells. Upregulation and/or

dysregulation of cytokines in inflamed tissue may be directly or

indirectly responsible for exacerbation of chronic inflammatory

diseases. Introduction of the chimeric nucleotide to activated

inflammatory cells causes them to undergo apoptosis. Pharmaceutical

compositions of the chimeric nucleotide may be useful for treating

inflammatory disorders such as multiple sclerosis, Crohn's disease,

clinflammatory disorders such as multiple sclerosis, Crohn's disease,

ulcerative colitis, psoriasis, graft versus host disease, lupus

erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing

spondylitis, and in particular, rheumatoid arthritis. The use of such

chimeric nucleotides offers simpler and cheaper long-term relief, in
splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a cis-acting nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oid arthritis. The use of sucheaper long-term relief,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation; chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis; psoriasis; graft versus host disease; lupus erythematosus; diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          olynucleotide consisting of a tumour necrosis factor an apoptosis-inducing Granzyme B polynucleotide -
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2.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                            standard; DNA;
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(Updated on 25-MAR-2003 to correct PR field.)
   invasive
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comparison with existing conventional pharmaceutical methods.
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                                                              Score 43; DB 20
Pred. No. 36-07;
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Pred: No: 3e-0
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                                         G; 221
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                                         C; 172
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07-FEB-1986;
17-JUL-1986;
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20-JAN-1991
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standard; DNA;

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The polypeptide is cytotoxic to human tumor cells but not to normal cells. They are also cytotoxic to primary cell cultures obtained from metastasis lesions of patients suffering from striated muscle tumors. They are also resistant to all chemotherapeutic agents. See also AAN70073-75, AAP70077-78 and AAP95592. (Updated on 25-MAR-2003 to correct PR field.)
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                                                              100.0%;
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86JP-0024220.
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43; Conservative
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Best Local Similarity 100
Matches 43; Conservative
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                                                                                    Acute leukaemia cell; THP-1; anti-tumour agent; ss
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Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 43; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                            Intrinsic TNF prodn. derivation agents - at least one of which has TNF activity.
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21-SEP-1990
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05-JUL-1984;
05-JUL-1984;
03-DEC-1984;
03-DEC-1984;
25-JUL-1984;
03-DEC-1984;
                                                                 by
 15-OCT-1984;
07-FEB-1985;
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                               Mark DF,
                  (CETU)
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                                                                                                                                                                                                                Score 43; DB 10;
Pred. No. 3.2e-07;
Mismatches 0
                                                                                                                                                                                                     C; 340 G; 253 T;
                                                                                                                                                                                         field.)
                                                 agent;
                                                                                                                                                                                         (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                            Gene for anticarcinogenic peptide. It
                                                                                                                                               wel DNA, plasmid and polypeptide(s) useful as anticarcinogenic agents
                                   for anti-cancer peptide
                                                agent; anti-cancer
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1..474
/*tag= a
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                                                                                                                                                                 ?; 17pp; Japanese
                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                     Sequence 1200 BP; 278 A; 329
                                                                                                                                                                                                                                                                                   AAN60558 standard; DNA; 1275
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82US-0435154.
83US-0486162.
83US-0564224.
                                                                                                87JP-0252174
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                         entry)
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                                                                                                                                                                                                                             Conservative
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                  (updated)
(first en
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                                                                                                                                    WPI; 1989-154899/21.
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Best Local Similarity
Matches 43; Conser
                                                Anticarcinogenic
                                                                                                                                                                                                                                                                                                                       Sequence encodin
Ser 69 in pAW731
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19-OCT-1982;
15-APR-1983;
20-DEC-1983;
                                   Part of gene
                                                                       JP01095784-A
                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                               06-OCT-1987;
                                                                                                           06-OCT-1987;
                                                            THP-1 cells.
                                                                                                                                                                 Fig 2; Page
                                                                                                                        SEN
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                  25-MAR-2003
11-MAR-1990
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                                                                                                                                              DNA,
      AAN90969;
                                                                                                                        (SENG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
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                                                                                                                                                                      New synthetic muteins of human tumour necrosis factor protein are obtd. by direct mutagenesis and retain antitumour activity
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3.2e-07;
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Pred. No. 3.26
0; Mismatches
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Secretory leader
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..534
/*tag= a
1..60
/*tag= b
/label= Secretory les
61..534
/*tag= c
                                                                                    Wang AM;
                                                                                                                                                                                                                       47pp; English
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Similarity 100.0%;
43; Conservative (
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84US-0627959.
84US-0628069.
84US-0677156.
84US-0677156.
84US-0677257.
84US-0661026
85US-0695934
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                                                                                   SDY,
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                                                                                                               WPI; 1986-225458/34.
P-PSDB; AAP60656.
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                                                                                                                                                                                                                     Disclosure; Fig
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                                                  CETUS
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Sequence encodes the pure human tumour necrosis factor, mutants which are covered by the claims. TNF and mutants are useful in treating tumours, especially in tandem with interferon. The encoding sequence may be used to create plasmid pTrpXAPTNF, allctransformation of an E.coli host for the expression of TNF.
                                                                                                                                  Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 other;
                                                                                                                                                                             CAAACTGGGGCCTCCAGAACTCACTGGGGC
                                                                                                                                               th Similarity 100.0%; 43; Conservative 0;
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and transformed
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       INC.
                    SH,
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                                 WPI; 1986-015483/03
P-PSDB; AAP60417.
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                     Lee
       GENENTECH
                                                                            Fig
                     Aggarwal BB,
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                                                              seguences
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                                                                           Claim 20;
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Best Local S
Matches 43
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AAF21085
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TCAAACTGGGGCCTCCAGAACTCACTGGGGGCCTACAGCTTTGA

standard; DNA;

entry)

oligonucleotide related sequence antisense

nitis; Low adenosine antisense oligonucleotide; phosphorothicate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinit pulmonary hypertension; emphysema; pulmonary transplantation rejectic chronic obstructive pulmonary disease; pulmonary infection; bronchiti cancer;

WO200062736-A2

26-OCT-2000.

2000WO-US08020 24-MAR-2000;

99US-0127958 06-APR-1999;

EAST CAROLINA 3 NYCE VIND (UYEC-)

Nyce JW;

2000-679539/66 WPI; Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for tracancers and respiratory obstructions -

English 1592pp; Page 887; Disclosure;

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antinfinamatory, analgesic, immunosuppressive, antisthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, brankylmin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide transmitters, defensine, growth factors, vasocative peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, and/or surfactant hypoproduction which are associated with a disease (CDE), pain, cystic fibrosis (CP), allergic thinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation respiratory pulmonary inflammation, and/or cancer Abriles, and/or cancer Abriles, are present human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention. ö Gaps ö Length 1324; Indels 797 other; rcalacticecerceacaacticacteceeecctacaectitea ô 331 T; 0 Score 43; DB 21; Pred. No. 3.3e-07 Mismatches 0 Sequence 1324 BP; 298 A; 387 C; 308 G; | TCAAACTGGGGCCTCCAGAACTCACT 0 ; 100.08; 100.0%; Similarity 100 43; Conservative Н Query Match Best Local (Best Loc Matches ठ

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Indels

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Score 43; DB 7; Pred. No. 3.3e-07; Mismatches 0;

Length 1323;

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DNA

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mutant

or and cells.

English.

Nedwin GE;

Goeddel DV,

RESULT 13 **AAA**34963

1324 standard; DNA; AAA34963

ВР

AAA34963;

(first entry) 28-JUL-2000

ID NO:2652 SEO related polynucleotide Human adenosine receptor

asthma; COPD; Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway lung disease; ischaemic condition; pulmonary vasoconstriction; asthrespiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD, cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2

24-FEB-2000

99WO-US17712 03-AUG-1999;

98US-0095212 03-AUG-1998;

CAROLINA EAST UNIA (UXEC-)

371

us-09-801

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The present invention describes a new composition comprising an antisense oligonucleotide (NN) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired alivawys, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating asthma, impeded respiration, respiratory distress syndrome, pain, cystic asthma, impeded respiration, respiratory distress syndrome, pain, cystic asthma, impeded respiration, emphysema, chronic obstructive pulmonary disease (CoPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breat and prostate cancer. The A-containing ONS break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA33313 to AAA35312 represent the invention, which correspond to SEQ ID NO: 1 to 185, but the sequences are also called SEQ ID NO: 1 to 185, but the sequences are also called SEQ ID NO: 1 to 185, but the sequences (Invention, N B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: equences
                                                               New antisense oligonucleotides useful for treating e.g. pulmonary
vasoconstriction, inflammation, allergies, asthma, hypertension,
bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1324;
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Pred. No. 3.3e-07;
; Mismatches 0;
                                                                                                                                                Disclosure; Page 814-815; 1343pp; English.
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86..313
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314..787
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43; Conservative
                                  WPI; 2000-205971/18.
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cell;
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                                                                                                                                                       A human TNF protein which is modified from the sequence shown in AAP80728, including naturally ocurring allelic variants is claimed. claimed are: recombinant DNA sequences encoding the protein (AAN802 and control sequences for expression; a vector; a transformed host a method of producing the protein by culturing the host cell; pharmaceutical compsn. of the protein and a carrier and a method of treating tumour burden with the compsn. The muteins are capable of range of biological activities exhibited by native TNF but exhibit improved stability and ease of purification.
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                                                                                                            stability
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                                                                                                           with improved
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Pred. No. 3.3e-07;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     mature human tumour necrosis
                                                                                                                                                                                                                                                           G; 366 T;
                                                 Yamamoto R;
                                                                                                                                        1-2; 51pp; English.
                                                                                                 muteins -
                                                                                                                                                                                                                                                           C; 381
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86..313
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0
                                                 Lin LS,
                                                                                               Human tumour necrosis factor having comparable biological and ease of purification
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82US-0435154,
83US-0486162,
83US-0564224,
84US-0661026,
85US-0695934,
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          87US-0019221
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314..787
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P-PSDB; AAP80728.
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19-OCT-1982;
15-APR-1983;
20-DEC-1983;
15-OCT-1984;
07-FEB-1985;
         26-FEB-1987;
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WPI; 1986-225458/34 P-PSDB; AAP60655.

The sequence encoding TNF produced by the promyelocytic leukemia cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (see AAN60557). Neither of the cysteine residues (69 and 101 the TNF sequence appears to be involved in disulphide linkages. The patentors claim a novel synthetic mutein of a biologically active hTNF protein, having at least one cysteine residue free from a disulphide link and non-essential to the activity and having at least one of the cysteine residues deleted or replaced by another APlasmid pAW731 (Ser 69) is claimed. New synthetic muteins of human tumour necrosis factor protein are obtd. by direct mutagenesis and retain antitumour activity Disclosure, Fig 1; 47pp; English.

Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 other;

Gaī ô Length 1585; Query Match Best Local Similarity 100.0%; Pred. No. 3.4e-07; Matches 43; Conservative 0; Mismatches 0; Indels

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3, 2004, 04:47:56 Search completed: February Job time : 120.054 secs

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the number of results predicted by chance to have a than or equal to the score of the result being printed, I by analysis of the total score distribution. Description SUMMARIES H DB Query Match Length

EX118951 EX1 CB528492 UI-1 CD370363 UI-1 CD367676 UI-1

BX118951 CB528492 CD370363 CD367676

4444 6444

474 630 645 688

1000.0

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Result No.

364761 UI-H- 368142 UI-H- 308256 UI-H- 528694 UI-H- 307062 UI-H- 307062 UI-H- 308777 UI-H- 368116 UI-H- 368129 UI-H- 368187 UI-H- 368187 UI-H- 368187 UI-H- 368187 UI-H- 368187 UI-H-	E ST371 5 UI - H 6 UI - H 7 UI - H 8 UI - H 8 UI - H 8 UI - H 10 C 83 G 10 DK 10 B 10 C 83 G 11 C 8 B 10	ear EST 10-FEB-2003 ns cDNA clone rata; Euteleostomi; nidae; Homo. sch, E., Peters, M., schung GmbH ermany Ina Rolfs schung GmbH
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of I

CDNA Library Arrayed by: Dr. M. Bento Soares, University of I

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 1-29, >AT_rich#Low_complexity (matched compliment)

205-279, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD
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1 (bases 1 to 630)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (C Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACAT
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UI-H-FT2-bjd-e-20-0-UI.81 NCI CGAP_FT2 Homo sapiens cDNA cl UI-H-FT2-bjd-e-20-0-UI 3', mRNA sequence.
CB528492
CB528492.1 GI:29388228
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 474;
                                         ie is available royalty-free from RZPD;
ZPD (clone@rzpd.de) for further information.
mer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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5.5e-21;
hes 0;
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Pred. No. 5.5
0; Mismatches
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998L124300;
                                                                                                               sapiens"
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100.0%; P1
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Homo sapiens
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                                                       contact RZPD
M13r, Primer
Tel: +49 30 3
Fax: +49 30 3
www.rzpd.de
This clone is
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="mrnA"
/db xref="taxon:9606"
/clone="UI-H-FT2-bjd-e-20-0-UI"
/tissue_type="Adult"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/clone lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of lowa.
TAG_LIB=UI-H-FT2
TAG_LIB=UI-H-FT2
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_TSSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCGG"
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1 (bases 1 to 645)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP)
Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I cDNA Library preparation: Dr. M. Bento Soares, University of Io CDNA Library Arrayed by: Dr. M. Bento Soares, University of Io DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA sequence: 294-368, > (TAAA) n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
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UI-H-FT1-bkb-n-03-0-UI.81 NCI CGAP FT1 Homo sapiens
UI-H-FT1-bkb-n-03-0-UI 3', mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bkb-n-03-0-UI"
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/lab host="DH10B (Life Technologies)"
/clone lib="NCI CGAP FTI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG ILB=UI-H-FT1

TAG ILB=UI-H-FT1
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 688)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Lumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CONA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution in/Cgap.html

The following repetitive elements were found in this cDNA

sequence: 69-143, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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UI-H-FT1-bjr-l-14-0-UI.81 NCI CGAP FT1 Homo sapiens
UI-H-FT1-bjr-l-14-0-UI 3', mRNA sequence.
CD367676

CD367676.1 GI:31151766
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6.3e-21;
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Pred. No. 6.3
; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
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llarity 100.0%;
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Watches 104; Conser
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/tione=_u_n_n_rii=_uji_n_n_n_n_n
/tissue_type="Adult"
/dev_stage="Adult"
/lab_host="Dulub (Life Technologies)"
/lab_host="Dulub (Life Technologies)"
/clone lib="NCI CGAP FTI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
NCI CGAP FTI is a normalized convalibrary was normalized according to Enaldo, Lennon and Soares, Genome a pool of 81 kNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of lowa.

TAG_IISSUE=Human Lung Aveolar Macrophage

TAG_ESEQ-GGCCATGCCG"

TAG_ESEQ-GGCCATGCCG"

TAG_ESEQ-GGCCATGCCG"
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtain

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 296-370, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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1 (bases 1 to 696)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished
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UI-H-FT1-bhu-n-04-0-UI.81 NCI CGAP FT1 Homo sapiens
UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.
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Pred. No. 6.4e-21;
); Mismatches 0;
clone="UI-H-FT1-bjr-1-114-0-UI"
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__type="mRNA"
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larity 100.0%;
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Query Match
Best Local Similarity
Matches 104; Conser
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                                 /tissue_type="Aveolar Macrophage"
/dev_stage="Aveolar Macrophage"
/dev_stage="Aveolar Macrophage"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT1
TAG_LIB=UI-H-FT1
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"
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CDNA clone
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

| (bases 1 to 699)
| NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
| National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
| Unpublished
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Ic

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Icwa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Icwa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Icwa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 296-370, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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UI-H-FT2-bjm-j-11-0-UI.s1 NCI CGAP FT2 Homo sapiens UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.
CD364761
CD364761.1 GI:31148851
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Pred. No. 6.5e-21;
); Mismatches 0;
xref="taxon:9606"
ne="UI-H-FT1-bhu-n-04-0-UI"
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/organism="Homo sapiens"

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703 bp mRNA linear EST 29-MAY-2003
NCI CGAP FT1 Homo sapiens cDNA clone
, mRNA sequence.
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1 (bases 1 to 703)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
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Email: cgapbs-r@mail:nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Ic

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Ic

DNA Sequencing by: Dr. M. Bento Soares, University of Ic

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 298-372, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLVA=Yes.
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/db_xref="taxon:9606"
/clone="UI-H-FT1-bjv-e-20-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies
/clone_lib="NCI_CGAP_FT1"
                                                                                                                                                                                                                                                                                                                                                                         core 104; DB 14;
red. No. 6.5e-21;
Mismatches 0;
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UI-H-FT1-bjv-e-20-0-UI 3', mRi
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larity 100.0%;
Conservative
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Homo sapiens
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of lowa.
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CA308256.1 GI:24471310
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SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom:

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 713)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CONA Library preparation: Dr. M. Bento Soares, University of Iov

DNA Library preparation: Dr. M. Bento Soares, University of Iov

DNA Sequencing by: Dr. M. Bento Soares, University of Iow

Clone Distribution: Clone distribution information can be obtaif

from Dr. M. Bento Soares, bento-soares@ulowa.edu

The following repetitive elements were found in this cDNA

Sequence: 296-370, > (TAAA) n#Simple_repeat

Seg primer: M13 FORWARD

POLYA=Yes.
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TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"
TAG_SEQ=GGCCATGCCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-e-14-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 6.5e-21;
Matches 104; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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CA308256/c
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AUTHORS
TITLE
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/CIONE_IID="NCI_CARF_FII"
//OCCE="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_LIB=UI-H-FT1

TAG_LIB=UI-H-FT1

TAG_LIB=UI-H-FT1

TAG_ENSUE=Human Lung Aveolar Macrophage

TAG_SEQ=GGCCATGCCG"

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 719)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CONA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA sequence: 294-368, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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/db_xref="taxon:9606"
/clone="UI-H-FT2-bjd-1-22-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core 104; DB 14;
red. No. 6.5e-21;
Mismatches 0;
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-H-FT2-bjd-1-22-0-UI.81 NCI CGAP FT2 Hc
-H-FT2-bjd-1-22-0-UI 3', mRNA sequence.
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|larity 100.0%;
| Conservative (
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Homo sapiens
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Best Local Similarity
Watches 104; Conser
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UI-H-FT2-bj
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CB528694.1
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AUTHORS
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Location/Qualifiers

1. .722

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5846517"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_EII"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_EII"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_l: BcoR I; Site_2: Not I;
NCI_CGAP_EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 722)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CONA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CLONE Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov

The following repetitive elements were found in this CDNA

Sequence: 297-371, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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                                        with
         / Lab_nost="Dailor (Line Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) wit]
modified polylinker; Site_l: ECOR I; Site_2: Not I;
NCI_CGAP_FT2 is a subtracted cDNA library constructed
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
subtracted according to Bonaldo, Lennon and Soares, G
Research, 6:791-806, 1996. The tissue was provided by
Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT2

TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"

3 a 163 g 188 t 2 others
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Technologies) "
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Pred. No. 6.6e-21;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T22 bp mRNA UI-H-EI1-azb-j-22-0-UI.s1 NCI_CGAP_EI1 FIMAGE:5846517 3', mRNA sequence.
BQ007008
BQ007008.1 GI:19731908
EST.
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l Similarity 100.0%;
104; Conservative (
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Best Local S
Matches 104
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ORIGIN
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BQ007008/c
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AUTHORS
TITLE
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synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the ACACTTGCAC.

TAG_LIB=UI-H-EII
TAG_LIB=UI-H-EII
TAG_LISSUE=chondrosarcoma
TAG_SEQ=ACACTTGCAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2002
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of Iowa
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1 (bases 1 to 722)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-o-04-0-UI"
/tissue_type="Aveolar Macrophage"
/dev stage="Adult"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of I

CDNA Library Arrayed by: Dr. M. Bento Soares, University of I

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obt

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 295-369, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD
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Mismatches 0;
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Pred.
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primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG LIB=UI-H-FTI
TAG LIB=UI-H-FTI
TAG SEQ=GGCCATGCCG"
)3 a 165 c 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD364988
UI-H-FT2-bjn-c-04-0-UI.81 NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.
CD364988.1 GI:31149078
EST.
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1 (bases 1 to 722)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iova
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 297-371, > (TAAA) n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
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/clone lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia)
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT2 is a subtracted cDNA library construct
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-c-04-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies
                                                                                                                                                                                                                                                                                                                                                                                 Score 104; DB 14;
Pred. No. 6.6e-21;
0; Mismatches 0;
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COMMENT

FEATURES

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Homo Bapiens

Butheria; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 723)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained
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subtracted according to Bonaldo, Lennon and Soares, Research, 6:791-806, 1996. The tissue was provided Gary W. Hunninghake of the University of Iowa. TAG_LIB=UI-H-FT2
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"
                                                                                                                                                                                                                                                                                                                                                                          AAP_FT1 Homo sapiens cDNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this
sequence: 297-371, > (TAAA) n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                   104
                                                                                               others
                                                                                                                                                                                                      GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGAT
                                                                                                                                            Length
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                                                                                                                                         Score 104; DB 14;
Pred. No. 6.6e-21;
); Mismatches 0;
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UI-H-FT1-bhy-b-23-0-UI 3', mRNA
CA308777
CA308777.1 GI:24471831
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0
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                                                                                                                                       Query Match
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Matches 104
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Location/Qualifiers

Location/Qualifiers

Lorganism="Homo sapiens"

/ organism="Homo sapiens"

/ db xref="taxon:9606"

/ clone="UI-H-FT1-bjv-a-04-0-UI"

/ tissue_type="Aveolar Macrophage"

/ dev stage="Adult"

/ lab_nost="DH10B (Life Technologies)"

/ lab_nost="DH10B (Life Technologies)"

/ clone lib="NCI CGAP FT1"

/ clone lib="NCI CGAP FT1"

/ note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;

NCI CGAP FT1 is a normalized cDNA library constructed from a pool of E1 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soarbes, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.

Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pyT7T3-Pac vector. The oligonucleotide used to prime the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Ic

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Ic

DNA Sequencing by: Dr. M. Bento Soares, University of Icwa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 297-371, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
and tis
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Catarrhini, Hominidae, Homo.
                    sequence that is located between the Not I site (dT)18 tail. The sequence tag for this library i GGCCATGCCG. The tissue was provided by Dr. Gary Hunninghake of the University of Iowa.

TAG_LIB=UI-H-FT1

TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"

164 g 191 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Eute. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom 1 (bases 1 to 723)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project Unpublished
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FT1 Homo sapiens
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                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CD368116 723 bp mRNA
UI-H-FT1-bjv-a-04-0-UI.s1 NCI CGAP FT1 Homc
UI-H-FT1-bjv-a-04-0-UI 3', mRNA sequence.
CD368116
CD368116.1 GI:31152206
EST.
Homo sapiens (human)
                                                                                                                                                                                                                                                    Score 104; DB 14;
Pred. No. 6.6e-21;
); Mismatches 0;
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l Similarity 100.0%;
104; Conservative (
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Best Local
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CD368116/C
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AUTHORS
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COMMENT

SOURCE

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/organism="Homo sapiens"
/mol_type="mkNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="Ul-H-FT1-bic-b-17-0-Ul"
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/lab_host="DH10B (Life Technologies)"
/lab_host="Macrophage"
/lab_host="Macroph
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FT1 Homo sapiens cDNA clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of CDNA Library Arrayed by: Dr. M. Bento Soares, University of I

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obt

from Dr. M. Bento Soares, bento-soares@ulowa.edu

The following repetitive elements were found in this cDNA

sequence: 297-371, > (TAAA) n#Simple_repeat
synthesis of first-strand cDNA contains a library sequence that is located between the Not I site an (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_LIB=UI-H-FT1

TAG_TISSUE=Human Lung Aveolar Macrophage

TAG_SEQ=GGCCATGCCG"
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Pred. No. 6.6e-21;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     724 bp mRNA
UI-H-FT1-bic-b-17-0-UI.81 NCI CGAP FT1 H
UI-H-FT1-bic-b-17-0-UI 3', mRNA sequence
CA309711
CA309711.1 GI:24472765
EST.
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pT7T3-Pac vector. The oligonucleotide used to prime synthesis of first-strand cDNA contains a library ta sequence that is located between the Not I site and (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_LIB=UI-H-FT1

TAG_LISSUE=Human Lung Aveolar Macrophage

TAG_SEQ=GGCCATGCCG"

190 t 1 others
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BASE COUNT ORIGIN

Gaj **;** 0 Indels Ouery Match Best Local Similarity 100.0%; Pred. No. 6.6e-21; Matches 104; Conservative 0; Mismatches 0;

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724;

Length

GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 595 595 61 a a ઠ

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06:12:17 2004, m Search completed: February Job time: 2472.58 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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leic - nucleic search, using sw model	February 3, 2004, 03:36:36; Search time 450.769 Seconds (without alignments)	US-09-801-371A-2 t score: 43 ce: 1 tcaaactggggcctccagaaactgggggcctacagctttga 43	g table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	ed: 2888711 seqs, 20454813386 residues	number of hits satisfying chosen parameters: 5777422	m DB seq length: 0 m DB seq length: 200000000	sing: N	GenEmbl: * 1: gb_ba: * 2: gb_htg: * 5: gb_on: * 6: gb_pat: * 7: gb_pat: * 10: gb_br: * 11: gb_br: * 11: gb_br: * 11: gb_br: * 12: gb_br: * 13: gb_un: * 14: gb_ur: * 15: em_ba: * 16: em_ba: * 17: em_ba: * 18: em_htg: * 29: em_ov: * 20: em_ov: * 20: em_ov: * 21: em_btg: * 22: em_bt: * 23: em_htg_inv: * 33: em_htg_mus: * 34: em_htg_man: * 35: em_htg_man: * 36: em_htg_other: * 36: em_htg_other: * 37: em_htg_man: * 38: em_htgo_hum: * 39: em_htgo_hum: * 39: em_htgo_hum: * 39: em_htgo_hum: * 39: em_htgo_hum: *
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72 degrees C
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Unclassified.

1 (bases 1 to 787)

Tatake, R.J., Marlin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory
Patent: US 6537784-A 7 25-MAR-2003;
Location/Qualifiers
     Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: CACTAAGAATTCAAACTGGGC
Primer B: GAGGAAGGCCTAAGGTCCAC
STS size: 166
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/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/map="6"

/clone_lib="Human"

210 .375

210 .231

complement (356 .375)
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BD070551
Self-regulated apoptosis of inflammatory cells by gene therapy.
BD070551
BD070551.1 GI:22616154
JP 2001516210-A/13.
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1 (bases 1 to 787)

Tatake, R.J., Marlin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy Patent: JP 2002504381-A 7 12-FEB-2002;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
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Self-regulated apoptosis of inflammatory cells by gene therapy
BD137681
BD137681.1 GI:23232626
JP 2002504381-A/7.
Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 787)
Tatake, R.J., Marlin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory cells by Patent: JP 2001516210-A 13 25-SEP-2001;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
OS Unidentified
PN JP 2001516210-A/13
PD 25-SEP-2001
PF 27-FEB-1998 JP 1998537909
PR 28-FEB-1997 US 60/039266
PI REVATI J TATAKE, STEVEN D MARLIN, RANDALL W BAR A61K31/70, C07H21/04, C12N15/12, C12P19/34
CC Strandedness: Single;
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Location/Qualifiers

1. .787
/organism="unidentified"
/wol_type="genomic DNA"
/db_xref="taxon:32644"
a _204 c 172 g 221 t
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Score 43; DB 6; Pred. No. 6.3e-07; Mismatches 0;
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Topology: Linear;
TNF alpha nontranslated region
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PD 12-FEB-2002
PP 12-JAN-1999 JP 2000533579
PR 27-FEB-1998 US 60/076316
PI REVATI J TATAKE, STEVEN D MARLIN, RANDALL W BARTON PC
C12N15/09, A61K31/7088, A61K48/00, A61P1/04, A61P3/10, A61P17/06, PC
A61P25/00,
PC A61P29/00, A61P43/00, C12N9/64, C12Q1/68//C12N5/10, C12N15/00,
C12N5/00
CC TNF-alpha untranslated region
FH Key Location/Qualifiers
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FT Source /Organism='Homo sapiens (human)'.
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Mammalia, Eutheria, Primates, Catarrhini, Homin
1 (bases 1 to 817)
Soma, G.I., Mizuno, D., Tsuji, Y. and Kobayashi, N.
Anti-aids preparation
Patent: EP 0450240-A 9 09-OCT-1991,
Soma, Gen-Ichiro, Mizuno, Den'ichi
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Pred. No. 6.3e-07;
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mol_type="genomic DNA"
db_xref="taxon:9606"
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mol_type="genomic DNA"
db_xref="taxon:9606"
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fragment from THP-I
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DNA sequence coding for ant:
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E02109.1 GI:2170351

JP 1989256390-A/1.
Glycine max (soybean)
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Submitted (24-SEP-1999) Farhan A.J., CID-Immunology Research
Division, Manchester University, Medical School, Stopford Building
Oxford Road, Manchester, M13 9PT, UNITED KINGDOM
Location/Qualifiers
                                                       Soma, G., Mizuno, D. and Tsuji, Y.

Soma, G., Mizuno, D. and Tsuji, Y.

NOVEL DNA AND PRODUCTION THEREOF, NOVEL PLASMID HAVING SAME, NOVEL POLYPEPTIDE AND PRODUCTION THEREOF AND NOVEL ANTINEOPLASTIC AGENT FROM SAID POLYPEPTIDE

PROM SAID POLYPEPTIDE

PROM GENICHIRO, MIZUNO DENICHI

PN JP 1989256390-A/1

PD 12-OCT-1989

PF 03-APR-1988 JP 1988081683

PI SOMA GENICHIRO, MIZUNO DENICHI, TSUJI YOSHIAKI PC

C12N15/00, A61K37/24, C07K13/00, C12P21/02, (C12P21/02, C12R1:19); CC

strandedness: Double;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Catarrhini; Hominidae; Homo
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   /product='Anti-tumor polypeptide'
Location/Qualifiers</pre>
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Identification of new rare variant of human TNF-alpha
Unpublished
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AJ249755.1 GI:6002308
TNF-alpha gene; tumor necrosis factor-alpha.
Homo sapiens (human)
Homo sapiens
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/country="United Arab Emirates"
/note="new rare variant"
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Homo Bapiens TNF-alpha gene for tumor
UTR, country United Arab Emirates.
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Pred. No. 6.2(); Mismatches
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/organism="Glycine max"
/mol_type="genomic DNA"
/db_xref="taxon:3847"
a _268 c 206 g 16
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hypothetical: No;
anti-sense: No;
*source: library=THP-1
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1 (bases 1 to 1323)
Aggarwal, B.B., Lee, S.H., Goeddel, D.V. and Nedwin, G.E.
Tumor necrosis factor, methods for its preparation, compositions containing it, DNA encoding it and assay method using such DNA Patent: EP 0168214-A2 6 15-JAN-1986;
Location/Qualifiers
1. 1323
/organism="unknown"
298 a 387 c 308 g 330 t
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Unclassified.

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I (bases 1 to 1275)

Mark, D.F., Lin, L.S., Lu, S.-D.Y. and Wang, A.M.

CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUM
NECROSIS FACTOR PROTEINS
NECROSIS FACTOR PROTEINS
L Patent: WO 8604606-A 5 14-AUG-1986;
Location/Qualifiers
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Pred. No. 6.1e-07;
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Pred. No. 6e-07;
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from Patent WO 8604606
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from Patent EP 0168214
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/gene="TNF-alpha"
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Similarity 100.0%;
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., san, H.R. and Guren, E.N.

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Shomosapiens
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LON CDNA encoding human tumor necrosis factor.

N E00702.

E00702.1 GI:2168979

Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1324)

E 2 (bases 1 to 1324)

S Baraa, B.A., Debitsudo, B.G., San, H.R. and Guren, E.N.

TUMOR NECTROTIC FACTOR

L Patent: JP 1986040221-A 1 26-FEB-1986;

GENENTECH INC
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Location/Qualifiers
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/product='tumor
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Query Match Best Local S Matches 43

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DEFINITION ACCESSION VERSION KEYWORDS

RESULT 12 SYNTNFTRP LOCUS

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/codon_start=1
/codon_start=1
/transl_table=11
/protein_id="AAC42098.1"
/db_xref="GI:209486"
/translation="MSTESMIRDVELAEEALPKKTGGPQGSRRCLFLSLFSFL_Translation="MSTESMIRDVELAEEALPKKTGGPQGSRRCLFLSLFSFL_TreCLLHFGVMGPQREEFPRDLSLISPLAQAVRSSRTPSDKPVAHVVANPQQUNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQGCPSTHVLLTHTUSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINDFAESGQVYFGIIAL"
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/note="synthetic tumor necrosis factor signal 100. .876
/product="synthetic tumor necrosis factor" 438 c 336 g 287 t
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tumor necrosis factor.

synthetic construct
artificial sequences.

"E 1 (bases 1 to 1379)

S Nobuhara,M., Kanamori,T., Nagase,Y., Nii,A., Mor.
Tohyama,J., Andoh,S. and Kurimoto,M.
The expression of human tumor necrosis factor in
Nucleic Acids Symp. Ser. 17, 131-134 (1986)

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Original source text. ""
cDNA to mpw."
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to mRNA, clone pM324-346.
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/mol_type="mRNA"
/db_xref="taxon:32630"
1787.879
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Pred. No. 6e-07;
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 1 (bases 1 to 1324)
Aggarwal, B.B. and Lee, S.He.
Synergistic cytotoxic composition
Patent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco,
Location/Qualifiers
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1. .1585 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644" a 473 c 389 g 371

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Search completed: February 3, 2004, 05:13:54 Job time : 450.769 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Pred. No. 9.5e-25;
Mismatches 0;
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Tatake, R.J., Marlin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory
Patent: US 6537784-A 7 25-MAR-2003;
                 Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA
Tel: (650) 320-5801
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: CACTAAGAATTCAAACTGGGC
Primer B: GAGGAAGGCCTAAGGTCCAC
STS size: 166
PCR Profile:
Initial incubation: 94 degrees C
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/mol type="genomic DNA"

/db xref="taxon:9606"

/map="6"

/clone lib="Human"

210. .375
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PCR Cycles:
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PAT 18-SEP-2002 gene therapy.
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LUOISI6210-A 13 25-SEP-2001;

LUOISI6210-A 13 25-SEP-2001;

OS Unidentified

PN JP 2001516210-A/13

PD 25-SEP-2001

PF 27-FEB-1998 JP 1998537909

PR 28-FEB-1997 US 60/039266

PI REVATI J TATAKE, STEVEN D MARLIN, RANDALL W 1 A61K31/70, C07H21/04, C12N15/12, C12P19/34

CC Strandedness: Single;

CC TOPOlogy: Linear;

CC TNF alpha nontrans1-

FH Key

FT SOURCE
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/organism="unidentified"
/wol_type="genomic DNA"
/db_xref="taxon:32644"
a _204 c 172 g 221
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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us-09-801-371a

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TO S homosapiens
PN JP 1986040221-A 1 26-FEB-1986;

OS homosapiens
PN JP 1986040221-A/1

PD 26-FEB-1986

PP 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 677156, PR 05-JUL-1984 US 84 677257, 03-DEC-1984 US 84 677257, PR 05-JUL-1984 US 84 677257, 03-DEC-1984 US 84 677454 PI BARAA BUSHIYAN AGAMARU, DEBITSUDO BANNOOMAN GETSUDERU, PI SAN HII RII, PI GUREN EBAN NEDOUIN

PC COTH21/04,
PC COTH21/04,
PC CIZN15/00;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical...
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                      GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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Tumor necrosis factor, methods for its preparation, composition containing it, DNA encoding it and assay method using such DNA Patent: EP 0168214-A2 6 15-JAN-1986;
Location/Qualifiers
1. .1323
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CDNA encoding human tumor necrosis factor.

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E00702.1

GI:2168979

JP 1986040221-A/1.

Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Hom

1 (bases 1 to 1324)

Baraa, B.A., Debitsudo, B.G., San, H.R. and Guren, B.N.

TUMOR NECTROTIC FACTOR

Patent: JP 1986040221-A 1 26-FEB-1986;

GENENTECH INC
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104; Conservative 0;
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BD137681.1 GI:23232626
JP 2002504381-A/7.
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)

Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Bukaryote; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 787)
Tatake,R.J., Marlin,S.D. and Barton,R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy
Patent: JP 2002504381-A 7 12-FEB-2002;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002504381-A/7
PD 12-FEB-2002
PR 27-FEB-1998 US 60/076316
PR 27-FEB-1999 US 60/076316
PR 27-FEB-19
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Unclassified.
In (bases 1 to 1275)
Mark, D.F., Lin, L.S., Lu, S.-D.Y. and Wang, A.M.
CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUM
NECROSIS FACTOR PROTEINS
L Patent: WO 8604606-A 5 14-AUG-1986;
L Location/Qualifiers
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1. .1275
/organism="unknown"
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9.9e-25;
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ive 0; Mismatches 0;
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/mol_type="genomic DNA"
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_204 c 172 g 22:
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RESULT 5 108430 LOCUS DEFINITION ACCESSION VERSION KEYWORDS

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1 (bases 1 to 1402,
Lin,L.S. and Yamamoto,R.
Purification method for tumor necrosis farent: US 4677197-A 2 30-JUN-1987;
Cetus Corporation; Emeryville, CA
Location/Qualifiers

1. .1465
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Pred. No. 1e-24;
); Mismatches
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Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 104; Conservative 0; Mismatches
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E 1 (bases 1 to 1585)
AS Vile, R.G. and Hart, I.R.
TUMOUR THERAPY
IMP CANCER RES TECH (GB)
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Location/Qualifiers
1. 1585
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1 from Patent US 4677063.
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Sequence 12 from Patent WO9404196
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9.9e-25;
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Best Local Similarity 100.0%; Pred. No. 9.9e-25;
Matches 104; Conservative 0; Mismatches 0;
cell_type=promyelocytes;
cell_line=HL-60;
clone=lambda42-4, lambda16
Location/Qualifiers
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US 4650674.
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Unknown.
Unclassified.
1 (bases 1 to 1324)
Aggarwal, B.B. and Lee, S.He.
Synergistic cytotoxic composition
Datent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco, C?
Location/Qualifiers
1. 1324
/organism="unknown"
/organism="unknown"
/organism="unknown"
                                                       <1. .61
62. .532
/product='tumor
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CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
NECROSIS FACTOR PROTEINS
Patent: WO 8604606-A 3 14-AUG-1986;
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Molecular cloning of the complementary DNA for human tumor
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1 (bases 1 to 1585)

Mark, D.F., Wang, A.M., Ladner, M.B., Creasey, A.A., Van Arsdell
and Lin, L.S.

Human tumor necrosis factor

Patent: US 4677064-A 1 30-JUN-1987;

Cetus Corporation; Emeryville, CA

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Sequence 1 from Patent US 4677064.
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1 (bases 1 to 1585)
Mark,D.F., Wang,A.M., Ladner,M.B., C;
Arsdell,J.
Human tumor necrosis factor
Patent: US 4677063-A 1 30-JUN-1987;
Cetus Corporation; Emeryville, CA
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ALIGNMENTS

Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha tumour necrosis factor alpha; TNF-alpha; gene therapy; ss. Cis-acting nucleotide sequence derived from human TNF-alpha. Ben-Asouli Y; Jarrous N, 98IL-0126112. 98IL-0126757. ВР 99WO-IL00483. AAZ99816 standard; RNA; 104 (YISS) YISSUM RES & DEV CO entry) Osman F, (first WPI; 2000-257000/22 WO200014255-A1 Homo sapiens. 07-SEP-1998; 26-OCT-1998; 16-MAR-2000. 06-SEP-1999; 12-JUL-2000 Kaempfer R, AAZ99816; RESULT 1

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Example

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The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This cremoval is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the seplicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural present sequence represents a cis-acting nucleotide sequence of the
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Regulation of gene expression by mRNA splicing is carried out using cis-acting nucleotide sequence controlled by phosphorylation of the alpha-subunit of eukaryotic initiation factor 2
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                                                                                                                                                                                                                                                                                                                                                                    invention.
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Best Local S
Matches 104
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AAZ20979
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                                                                                                                                                                                                                                                                           and invasive surgery
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                                                                                                                                                                                                                             ankylosing
This sequence represents a human TNFalpha (tumour necrosis factor alpha 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were constructed comprising at least one TNFalpha promoter enhancer region (AAZ20975-Z20978), a TNFalpha promoter (AAZ20972-Z20974), a DNA encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNFalpha 3'UTR sequence. TNFalpha is one of a number of cytokines produced by inflammatory cells. Upregulation and/or dysregulation of cytokines in inflammed tissue may be directly or indirectly responsible for exacerbation of chronic inflammatory cells causes them to undergo apoptosis. Pharmaceutical inflammatory cells causes them to undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide may be useful for treating inflammatory disorders such as multiple sclerosis, Crohn's disease, lupus culcerative colitis, psoriasis, graft versus host disease, lupus erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis, and in particular, rheumatoid arthritis. The use of such chimeric nucleotides offers simpler and cheaper long-term relief, in chimeric nucleotides offers simpler and cheaper long-term relief, in chimeric nucleotides offers simpler and cheaper long-term relief, in
                                                    DNA
a
                                                                                                                                                                                                                                               such
                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTGATCCCTGACATCTG
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      factor al
, 220984)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATCTGGAGGACCATTGGTTCTGGCCAGAATGCTGC
                                                                                                                                                                                                                                                                                                                            0 other;
                                                                                                                                                                                                                                                                           comparison with existing conventional pharmaceutical
                                                                                                                                                                                                                                                                                                                                                       Score 104; DB 20;
Pred. No. 2.3e-25;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                          A; 204 C; 172 G; 221
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1..474
/*tag= a
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Local Similarity 100.0%;
Les 104; Conservative C
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82US-0435154.
83US-0486162.
83US-0564224.
84US-0661026.
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19-OCT-1982;
15-APR-1983;
20-DEC-1983;
15-OCT-1984;
07-FEB-1985;
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Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                       222
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Ser 69 in
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18-09

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The sequence encoding TNF produced by the promyelocytic leukemia cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) the TNF sequence appears to be involved in disulphide linkages. The patentors claim a novel synthetic mutein of a biologically active hTNF protein, having at least one cysteine residue free from a disulphide link and non-essential to the activity and having at least one of the cysteine residues deleted or replaced by another AA, Plasmid pAW731 (Ser 69) is claimed.
                                                                                                                                                                                                                                                                GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACAT
                                                                                                                                                                                                                                                                            GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACAT
                                synthetic muteins of human tumour necrosis factor protein obtd. by direct mutagenesis and retain antitumour activity
                                                                                                                                                                                              Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 other;
                                                                                                                                                                                                                                                                                                         Score 104; DB 7;
Pred. No. 2.7e-25;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secretory leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence encoding human tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 1..534
                                                               Disclosure; Fig 3a; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; interferon;
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 1323
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84US-0627959.
84US-0628060.
84US-0677156.
84US-0677257.
84US-0677257.
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/*tag=
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61..534
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WPI; 1986-225458/34
P-PSDB; AAP60656.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hTNF; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-DEC-1984;
05-JUL-1984;
05-JUL-1984;
03-DEC-1984;
03-DEC-1984;
25-JUL-1984;
03-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
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Best Local S
Matches 104
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104

Length 1275;

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human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antilnflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.
                                                                                                                                                                                                                                                                                           GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenosine antisense oligonucleotide related sequence #2652
                                                                                                                        the pure human tumour necrosis factor, mutants i by the claims. TNF and mutants are useful in especially in tandem with interferon. The may be used to create plasmid pTrpXAPINF, allow an E.coli host for the expression of TNF.
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                                                               new DNA coding
                                                                                                                                                                                                                                                                             GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGGCCTACAGCTTTGAT
                                                                                                                                                                                                                                                    Indelg
                                                                                                                                                                                                                            Length
                                                                                                                                                                                                   0 other;
                                                                                                                                                                                                                                                                                                                              Score 104; DB 7;
Pred. No. 2.7e-25;
); Mismatches 0;
                                                                                                                                                                                                    C; 310 G; 330 T;
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bronchoconstrict
                                                                mutant
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Ω,
                                                             or and cells.
                                                                                                 English
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  Goeddel
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                                                                                                                                                                                                   298 A; 385
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                                                               factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                               Pure tumour necrosis factores
sequences and transformed
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trigger adenosine receptor
cancers and respiratory ob
                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti sense
disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-679539/66.
                                                                                                                                   which are covered by treating tumours, esgencoding sequence may
                        WPI; 1986-015483/03
P-PSDB; AAP60417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                       Local Similarity
                                                                                                 Claim 20; Fig 10;
                                                                                                                                                                         transformation of
                                                                                                                                                                                                   Sequence 1323 BP;
                                                                                                                           encodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adenosine
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(NYCE/) NYCE
                                                             tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human low
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                                                                                                                          Sequence
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FEEFEEEXSXBXBXFXFXFXFXFXFXF
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides and a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating septide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokine and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adheaion molecules and their receptors, cytokine and chemokine receptors, and peripheral nervous and non-nervous system (CNS) and peripheral nervous and non-nervous system ceptides and receptors, binding proteins, adverbheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins and or surfactant hypoproduction which are associated with a disease or and/or bronchoconstriction and/or lung inflammation, allergy(ies) and/or bronchoconstriction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary transplantation rejection, pulmonary unfactions, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of heavenery invention
   1592pp; English
 Page 887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention
 Disclosure;
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other; 0 ۲. ۲ G; 331 308 ΰ 298 A; 387 1324 BP; Sequence

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Gaps
                                                       CCCTGACAT
                                                                                GAATICAAACIGGGGCCICCAGAACICACIGGGGCCIACAGCITIGAICCCIGACAI
                            · 0
   Length 1324;
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                                                       GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGGCCTACAGCTTTGAT
                            Indele
                                                                                                            GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC
                                                                                                                           GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC
Score 104; DB 21;
Pred. No. 2.7e-25;
; Mismatches 0;
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ch
il Similarity 100.0%;
104; Conservative
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  Query Match
Best Local
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(first entry)
     standard; DNA;
               28-JUL-2000
          AAA34963;
     AAA34963
  AAA34963
RESULT
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ВP

1324

Human adenosine receptor related polynucleotide SEQ ID NO:2652

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

WO200009525-A2 sapiens Ношо

24-FEB-2000

99WO-US17712 03-AUG-1999;

The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine. (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antinflammatory, antiallergic, and/or inflammation. The ON can have antinflammatory, antiallergic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired alivays, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces side effects. The A-containing ONS break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA35313 to AAA35312 represent the numberine sequences given in the sequences. SEQ ID NO:1 to 185, but the sequences of invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence of the present invention do not match up with their corresponding SEQ ID NO: sequences e.g. pulmonary hypertension, me, ischemia or New antisense oligonucleotides useful for treating e.gvasoconstriction, inflammation, allergies, asthma, hybronchitis, emphysema, respiratory distress syndrome, Page 814-815; 1343pp; English 98US-0095212 (UYEC-) UNIV EAST CAROLINA. 2000-205971/18. 03-AUG-1998; Disclosure; cancers

ö 9 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG Gaps ö 1324; Length Indels ; DB 21; 2.7e-25; hes 0; 100.0%; Score 104; I 100.0%; Pred. No. 2.: ive 0; Mismatches ö Conservative Similarity 104; Query Match Best Local S Matches 104 Н ò

1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

Sequence

gaatricaaacreegecerceagaacreacreegeceracageerrreareecergacarere GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 61 751

В

Sequence of pE4 encoding human tumour necrosis factor AAN80219 standard; DNA; 1560 28-DEC-1990 AAN80219; **AAN**80219 RESULT I HX S X M X B X B X X X X I

Location/Qualifiers Lymphokine; antitumour; ss sapiens Homo Key S

86WO-US00236

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03-FEB-1986;
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Matcl
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                                                                                                                                                                                                                                                                                cell;
                                                                                                                                                                                                                                                  nown in
s claimed. Als
in (AAN80219)
                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                           Ö
                                                                                                                                                                                                                                              A human TNF protein which is modified from the sequence shown in AAP80728, including naturally ocurring allelic variants is claimed. claimed are: recombinant DNA sequences encoding the protein (AAN802 and control sequences for expression; a vector; a transformed host a method of producing the protein by culturing the host cell; pharmaceutical compsn. of the protein and a carrier and a method of treating tumour burden with the compsn. The muteins are capable of range of biological activities exhibited by native TNF but exhibit improved stability and ease of purification.
                                                                                                                                                                                                                                                                                                                                                                                                           CCTGACATC
                                                                                                                                                                                                                                                                                                                                                                                         Gag
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                                                                                                                                                                                                                                                                                                                                                                                                                       in
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                                                                                                                                                                                      Human tumour necrosis factor muteins -
having comparable biological activity with improved stability
and ease of purification
                                                                                                                                                                                                                                                                                                                                                                      Length 1560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoding mature human tumour necrosis factor (hTNF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
                                                                                                                                                                                                                                                                                                                                                                                                           GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                  T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 104; DB 9; I
Pred. No. 2.8e-25;
                                                                                                                                         Yamamoto R;
                                                                                                                                                                                                                                                                                                                                                  G; 366
                                                                                                                                                                                                                              Disclosure, Fig 1-1 to 1-2; Slpp; English
                                                                                                                                                                                                                                                                                                                                                  C; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                       Lin LS,
                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                 Sequence 1560 BP; 340 A; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 1585
                                                                              88WO-US00183
                                                                                                87US-0019221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                     Ω
/*tag= a
314..787
/*tag= b
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/*tag= a
314.787
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anticancer;
                                                                                                                                       Thomson JW,
                                                                                                                                                          WPI; 1988-271165/38
P-PSDB; AAP80728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                    CETUS
                                                                                               26-FEB-1987;
                                       WO8806625-A.
                                                                             5-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
           mat peptide
                                                          07-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antitumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO8604606-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                      104;
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Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN60557;
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                                                                                                                                      Mark DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAN60557
                                                                                                                   (CETU)
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                                                                                                                                                                                                                                                                                            The sequence encoding TNF produced by the promyelocytic leukemia cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) the TNF sequence appears to be involved in disulphide linkages. The patentors claim a novel synthetic mutein of a biologically active hTNF protein, having at least one cysteine residue free from a disulphide link and non-essential to the activity and having at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                           stivity and having at or replaced by another AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor;
                                                                                                                                                                                                                     r necrosis factor protein retain antitumour activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
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2.8e-25;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour necrosis factor (TNF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 104; D. Pred. No. 2.8
                                                                                                                                                                                                                                                                                                                                                                                                  least one of the cysteine residues deleted Plasmid pAW731 (Ser 69) is claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; 389 G; 371
                                                                                                                                                                                                                      tumour
and re
                                                                                                                                           Wang AM;
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158..859
/*tag= a
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direct mutagenesis
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85US-0698939.
82US-0435154.
83US-0486162.
83US-0564224.
84US-0661026.
85US-0695934.
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P-PSDB; AAP60655.
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                                                                                                                                          Lin LS,
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                                                                                                                                                                                                                    synthetic
obtd. by d
                                                                                                            CETUS
07-FEB-1985;
19-OCT-1982;
15-APR-1983;
20-DEC-1983;
15-OCT-1984;
07-FEB-1985;
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07-AUG-1991
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                                                                                                                                       Mark DF,
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85US-0785847

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WPI; 1996-321849/32
 09-OCT-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUL-1996.
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Webster KA;
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under
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Best Local S
Matches 104
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                                                                              Prodn.
                  (BIOJ
                                  Allet
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AAT3102
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                                                                                                                                                                     TNF-like polypeptides and compsns. are produced by the fermentatio of host cells transformed with at least one DNA sequence which cod for a mammalian TNF-like polypeptide operatively linked to an expression control sequence in the transformed host.
(Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                              GAATICAAACIGGGGCCICCAGAACICACIGGGGCCIACAGCITIGAICCCIGACAI
                                                                                                                                                                                                                                                                                               GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor; TNF; phage T4; phage lambda; pL promoter; antitumour; anticancer; antimalarial; ss.
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                            Length 1606;
                                                                                                                                culturing
DNA
                                                                                                                                                                                                                                                                                                                 104
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                             other;
                                                                              Marmenout ALM;
                                                                                                                                                                                                                                                                                                                GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC
                                                                                                                                                                                                                                                                                                                          GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC
                                                                                                                                                                                                                                           ch 100.0%; Score 104; DB 7; I Similarity 100.0%; Pred. No. 2.8e-25; 104; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tumour necrosis factor cDNA clone p-hTNF-1
                                                                                                                                                                                                                             0
                                                                                                                                produced by recombinant
                                                                                                                                                                                                                           1606 BP; 357 A; 494 C; 394 G; 361 T;
                                                                            Tavernier JHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
158..859
/*tag= a
158..385
/*tag= b
386..856
/*tag= c
                                                                                                                               Mammalian tumour necrosis factors -
pro-karyotic hosts transformed with
                                                                                                                                                        9; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                            AAT15424 standard; cDNA; 1606
85US-0785847.
84US-0684595.
86WO-US02133.
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84US-0684595,
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                                                                             Fransen LM,
in J, Allet
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(first en
                                                                                                     WPI; 1986-182891/28
P-PSDB; AAP60531.
                                 BIOGEN NV.
FIERS W C.
ALLET B.
                                                           BIOGEN INC
                                                                             Fiers WC, Frans
VanDerHeyden J,
                                                                                                                                                         Example; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
09-OCT-1985;
21-DEC-1984;
09-OCT-1986;
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23-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-1985
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21-DEC-1984
                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 104
                                                                                                                                                                                                                                                                                               1075
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                                                                                                                                                                                                                             Sequence
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                                 (BIOJ )
(FIER/)
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1134
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                                                                                                                                                                                                                          A cDNA clone (AAT15424), p-hTNF-1 (DSM 3160), codes for the human tumour necrosis factor (hTNF) precursor (AAR88590). It was obtd. by screening a human cDNA library with a fragment of mouse TNF cDNA. The isolated cDNA may be linked to expression control sequences from phage T4 or phage lambda (see AAT15402-05 and AAT15425-26) for expression in host cells, esp. Escherichia coli, and commercial-scale prodn. of recombinant TNF of use as an antitumour, anticancer and antimalarial agent.
(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                       encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ischaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1606;
                                                                                                                                            control
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                                                                                                                       s factor - using recombinant DNA
T4 or lambda pL-T4 expression co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 other;
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2.8e-25;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 104;
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                                                                                                                         tumour necrosis factor
the control of T4 or 18
                                                                                                                                                                                               Example 9; Fig 9; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                            the control
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                                  Kawashima
                                                                   WPI; 1996-105230/11
P-PSDB; AAR88590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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BIOGEN
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reperfusion; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNF; apoptosis; ds; tumour; death domain receptor ligand; diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma; neurological malignancy; haematological malignancy; lichen planus; non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angioge malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour; T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid; discoid lupus erythematosus; human; gene; tumour necrosis factor.
                             HREE - partic. for tissue injury cause
                                                                                                            A PCR-generated DNA fragment (AAT31021) encoding human tumour necrosis factor (hTNF) (AAW00454). hTNF induces apoptosis and is not known to be induced by hypoxic stress. A -90 bp human metallothionein IIA promoter fragment (see also AAT31003) was inserted upstream of the hTNF gene and the construct was used to transfect mouse C2C12 myoblasts and A431 cells. Hypoxiamediated TNF induction and tumour control were demonstrated in an animal xenograft model.
                                                                                                                                                                                                                                                                         1643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour necrosis factor alpha (TNF alpha) DNA.
                                                                                                                                                                                                                                                                        Score 104; DB 17;
Pred. No. 2.9e-25;
; Mismatches 0;
                         Chimeric gene contg. therapeutic gene linked to expressing SOD etc. in hypoxic tissue to reduce by ischaemia or reperfusion
                                                                                                                                                                                                                                             Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha protein"
                                                                                   118pp; English
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153..854
/*tag= a
/product= "TNF alpha
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                                                                                                                                                                                                                                                                         100.0%;
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99US-149989P
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                                                                                     8; Page 100-101;
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA;
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20-AUG-1999;
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Best Local S
Matches 104
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P-PSDB;
                                                                                     Example
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This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking triepoxide. This method has cytostatic activity and works by blocking invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, had an alignancies, e.g. non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma, chronic lymphocytic leukaemia, malignant cutaneous Prcells, mycosis fungoides, non-MF cutaneous T-cell lymphoma, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered with other active agents, e.g. antimatastatic, anti-tumour or anti-angiogenic agents. The potent synergy between the diterpenoids and the death domain ligands allows increased killing at equivalent or lower doses, and can sensitise otherwise resistant cells. This sequence represents the human tumour necrosis factor alpha (TNF alpha) DNA. TNF alpha is a ligand for death domain receptors used in the used method of the invention in combination with diterpenoid triepoxides to kill tumours by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                     carcinoma
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                                       death domain receptor ligands of tumour cells -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 104; DB 24; Stailarity 100.0%; Pred. No. 2.9e-25; 104; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; 398 G; 380 T; 0
                                                                                                    20pp; English
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1..152
/*tag= a
852..1643
/*tag= b
                                       Use of a synergistic combination of diterpenoid triepoxides for killing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bb
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                                                                                                    Column 27-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis
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 P-PSDB; AAU75065
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                                                                                                    Disclosure;
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Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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The invention relates to a method for identifying a test compound that binds to a target RNA molecule, which comprises contacting a detectably labelled target RNA molecule with a library of test compounds under conditions that permit direct binding of the labelled target RNA to a member of the library of test compounds so that a detectably labeled target RNA:test compound complex is formed. The method is useful for screening libraries of compounds for those that are selectively bind to screening libraries of compounds for those that are selectively bind to a pre-selected target RNA. The compounds are useful for inhibiting the formation of a specific bound RNA:host cell factor complexes in vivo. They are also useful for treating or preventing diseases associated with overproduction or decreased protein function, such as amyloidosis, hammophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism, dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging, inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative disorders, Parkinson's disease or infections (bacterial, viral, fungal). The invention is also used in gene therapy. The present sequence is human tumour necrosis factor alpha (TNF-alpha) DNA. This sequence is the used to illustrate the method of the invention.
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molecule w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                  ig a test compound that binds to a target RNA more preventing amyloidosis, hemophilia, cancer, by contacting a detectably labeled target RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 398 G; 380 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATCTGGAGCCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 104; DB 25;
Pred. No. 2.9e-25;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 st RNA, target RNA:support-attached test (
spectrometry; high-throughput screening;
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                                                                                                                                                                                                                                                       Example, Page 53-54; 152pp; English.
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                                 2001US-282965P.
 11-APR-2002; 2002WO-US11757
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                                                                   THERAPEUTICS
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                                                                                                                                 WPI; 2003-075561/07
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Best Local Similarity
                                                                                                   Welch E;
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                                  11-APR-2001;
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                                                                                                                                                                   Identifying
treating or
                                                                   PTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104;
                                                                                                                                                                                                    diabetes,
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                                                                 (PTCT-)
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                                                                                                                                                                                                               The invention relates to a novel method for identifying a test compount that binds to a target RNA molecule comprising separating the detectablabeled target RNA: support attached test compound complex from uncomplexed target RNA molecules and test compounds. The separating process is carried out by flow cytometry and determining a structure of the type of test compound of the RNA: support attached test compound complex by mass spectrometry. The method is useful for high-throughput screening of libraries of compounds to identify pharmaceutical leads. This polynucleotide sequence represents a DNA sequence related to the detecting method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation; chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis; psoriasis; graft versus host disease; lupus erythematosus; diabetes; ankylosing spondylitis; rheumatoid arthritis; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                          test compound that binds to a target RNA molecule by detectably labeled target RNA:support-attached test ex from uncomplexed target RNA molecules and test
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                                                                                                                                                                                                                                                                                                                                                                                                                            ch 100.0%; Score 104; DB 25; Length 11 Similarity 100.0%; Pred. No. 2.96-25; Length 104; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= TNFalpha promoter
/note= "Human TNFalpha native promoter
740..1477
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;
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dipeptide a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)/ which was a limit
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/note= "Inactivating d
1490..2264
/*tag= c
/label= INFalpha 3'UTR
                                                                                                                                                                                        Example, Page 44-45; 131pp; English
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               INC
                                                                                                        Identifying a test compound separating the detectably la compound complex from uncomp
                                                                                                                                                         compounds by flow cytometry
               THERAPEUTICS
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                                             Almstead NG;
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               PTC
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               (PTCT-)
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12-JAN-1999;
                   27-FEB-1998;
                                                              Tatake RJ,
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98US-0076316 99WO-US00637

INGELHEIM (BOEH) BOEHRINGER

INC.

Barton RW; Marlin SD,

WPI; 1999-527630/44.

ic polynucleotide consisting of a tumour necrosis factor and an apoptosis-inducing Granzyme B polynucleotide chimeric promoter

12; 71pp; English 4; Fig Claim

This sequence represents chimeric nucleic acid -706TNFpGB3'UTR. This comprises at least one TNFalpha (tumour necrosis factor alpha) promote chancer region (AAZ20975-Z20978), a TNFalpha native promoter (AAZ20976) a DNA encoding a truncated form of the apoptosis-inducing Granzyme B protein (AAZ20979), and a TNFalpha 3'UTR (untranslated region) sequence (AAZ20979). TNFalpha is one of a number of cytokines produced by inflammatory cells. Upregulation and/or dysregulation of cytokines in inflammed tissue may be directly or indirectly responsible for exacerbation of chronic inflammatory diseases. Introduction of this chimeric nucleotide to activated inflammatory cells causes them to undergo apoptosis. Pharmaceutical compositions of this chimeric nucleotide may be useful for treating inflammatory disorders such as multiple sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus host disease, lupus erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis, and in particular, rheumatoid arthritis. The use of such chimeric nucleotides offers simpler and cheaper long-term relief, in comparison with existing conventional pharmaceutical and invasive surgery methods

Sequence 2270 BP; 556 A; 647 C; 545 G; 522 T; 0 other;

Gar 2270; .; 0 Length Indels Score 104; DB 20; Pred. No. 3.1e-25; ; Mismatches 0; Query Match Best Local Similarity 100.0%; F Matches 104; Conservative 0; GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATC GAATICAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATC 1705

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(c) 1993 - 2004 Compugen Ltd
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107 US-09-801-371A-1 104 1 gaattcaaactggggcctcc.....ggttctggccagaatgctgc Title: Perfect score: Sequence:

1.0 IDENTITY NUC Gaport Gapop 10.0 , Gapext Scoring table:

569978 seqs, 220691566 residues Searched:

1139956 hits satisfying chosen parameters Ğ O number Total

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued_Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being print and is derived by analysis of the total score distribution.

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	Description		equence 7, Appl	equence 36, App	4, Appl	equence 13, App	14, App	1, Appl	equence 1, Appl	34, App	7, Appl	3, Appl	1, Appl	Sequence 15, Appl	1, Appl	13, App	7, Appl	9, App1	39, App	1, Appl	82, App	equence 1004, A	30, App	equence 30, App	0, Ap	equence 29, Ap	equence 29, Ap	e 29,
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SUMMARIES	ΙD	-03	-22	-880-342-3	-50	-09-229-15	-09-229-15	-166-18	-09-313-932-	-09-109-663-	-09-341-587-	-09-818-512-	-09-169-768-	US-09-169-768-15	-08-655-086-	-09-169-76	-09-169-768-	94-691-60-	-09-484-970B	-08-159-784-	-09-328-111-8	-09-620-312D-	-08-911-853-3	-09-479-409-3	-09-479-453-3	-08-911-853-2	9-479-40	-479-453-2
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Patent No. 6329148
GENERAL INFORMATION:
APPLICANT: Rosen, Glenn
APPLICANT: Kao, Peter
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
TITLE OF INVENTION: Triptolides and Death Domain Ligands
FILE REFERENCE: SUN-109PRV2
CURRENT APPLICATION NUMBER: US/09/505,250A
CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNF cDNA HSTNFR (EMBL Accession #X01394)
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7.2e-27;
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Pred. No. 7.2e-27;
Mismatches 0
                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
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                   US/08/880,342
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V: 514
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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MOLECULE TYPE: DI
HYPOTHETICAL: NO
                                  FILING DATE: 2. CLASSIFICATION:
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SEQ ID NO 4
LENGTH: 1643
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Patent No. 6218179

GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Murphy, Brian
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Tassue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
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Pred. No. 5.7e-27;
Mismatches 0
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                                                                                                                                                                                RESULT 2
US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
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 Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
CITY: Palo Alto
STATE: CA
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
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Best Local Similarity 100.0%; P
Matches 104; Conservative 0;
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 Conservative
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 Gaps
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 Indels
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APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION
FILE REFERENCE: ISPH-0322
                                                                                                                  2065 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC
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 Mismatches
                                                                                                                                                                                            1, Application US/09166186A
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CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 1998-10-0
NUMBER OF SEO ID NOS: 250
 Conservative
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LOCATION: (2171)..(3381,
PUBLICATION INFORMATION:
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(1870)
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        Inflammatory Cells b
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                                                                    -1005TNFpGB3'UTR
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Pred. No. 8e-27;
0; Mismatches 0;
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Sequence 14, Application US/09229151C
Patent No. 6537784
GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Marlin, Steven D.
APPLICANT: Barton, Randall W.
TITLE OF INVENTION: Self-Regulated Apoptosis of Inf
FILE REFERENCE: 9/137
CURRENT APPLICATION NUMBER: US/09/229,151C
CURRENT FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: US 60/076,316
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 2.0
SEQ ID NO 14
LENGTH: 2570
TYPE: DNA
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Pred. No. 8.3e-27
                                                                                                                                  RESULT 5
US-09-229-151C-13
i Sequence 13, Application US/09229151C
i Patent No. 6537784
i GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Marlin, Steven D.
APPLICANT: Marlin, Steven D.
TITLE OF INVENTION: Self-Regulated Apoptosis of FILE REFERENCE: 9/137
CURRENT APPLICATION NUMBER: US/09/229,151C
CURRENT FILING DATE: 1999-01-12
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 2.0
SEQ ID NO 13
LENGTH: 2270
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Best Local Similarity 100.0%;
Matches 104; Conservative (
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OTHER INFORMATION: chimeric
-09-229-151C-13
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Best Local Similarity
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9-229-151C-14
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FEATURE:
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US-09-229-151C-14
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US-09-341-587-7/c

is Sequence 7, Application US/09341587

j Patent No. 6346606

j GENERAL INFORMATION:
    TITLE OF INVENTION: Protein Containing an SRCR Domain
    TITLE OF INVENTION Protein Containing an SRCR Domain
    TITLE REFERENCE: 4121-108
    CURRENT APPLICATION NUMBER: US/09/341,587
    CURRENT FILING DATE: 1999-08-31
    EARLIER FILING DATE: 1998-01-09
    NUMBER OF SEQ ID NOS: 12
    SOFTWARE: Patentin Ver. 2.1
    SEQ ID NO 7
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                                                Score 104; DB 3;
Pred. No. 9.2e-27;
Mismatches 0;
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Pred. No. 9.2e-2';
Mismatches
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il Similarity 100.0%; E
104; Conservative 0;
      1997-02-17
                                               ch 100.0%;
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FEATURE:
     ; DATABASE ENTRY DATE:
US-09-313-932-1
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; ORGANISM: Homo
US-09-341-587-7
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LENGTH: 3634
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                                  Gaps
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| Sequence 1, Application US/09313932A
| Patent No. 6228642
| GENERAL INFORMATION:
| APPLICANT: Baker, Brenda
| APPLICANT: Bennett, C. Frank
| APPLICANT: Butler, Madeline M.
| APPLICANT: Shanahan, William R.
| TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TWF-
| TITLE OF INVENTION: EXPRESSION
| FILE REFERENCE: ISPH-0356
| CURRENT FILING DATE: 1999-05-18
| NUMBER OF SEQ ID NOS: 501
                                                                                         2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACA
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    Length 3634;
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PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor genes: TITLE: structure, homology and chromosomal localization JOURNAL: Nucleic Acids Res.
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                                   Indels
                                                                                                                                              2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC
  Score 104; DB 3;
Pred. No. 9.2e-27;
Mismatches 0;
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PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910
                                                                                                                         GAATCTGGAGACCAGGGAGCCT
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  100.0%;
larity 100.0%;
Conservative 0
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ORGANISM: Homo sapiens
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Query Match
Best Local Similarity
Matches 104; Conser
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LOCATION:
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FEATURE:
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LOCATION:
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Gaps
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US-09-109-663-34
; Sequence 34, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
; APPLICANT: Tu, Guang-Chou
APPLICANT: Israel, Yedy
; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
; TITLE OF INVENTION: BFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 9855-301
; CURRENT FILING DATE: 1998-07-03
; CURRENT FILING DATE: 1997-07-03
; EARLIER APPLICATION NUMBER: 60/051,705
; EARLIER PILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.0
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us-09-801-371a-1

Version #1.30

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Patentin Release #1.0,
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BUECHTER, DOUGLAN
BROKAW, JANE
PHANG, GUANGHUI
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                                  APPLICATION DATA
                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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ADDRESSEE: DILWORTH
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                                                   APPLICATION NUMBER:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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US-09-169-768-1
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US-09-169-768-15
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APPLICANT:
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ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS,
THEREOF
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      Length 28720;
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US-09-169-768-1
; Sequence 1, Application US/09169768
; Patent No. 6492508
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
APPLICANT: BROKAW, JANE
; APPLICANT: BROKAW, JANE
; APPLICANT: PAOLELLA, DAVID
; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
                                                    Indels
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    Score 28; DB 4
Pred. No. 4.3;
0; Mismatches
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Pred. No. 11;
0; Mismatches
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US-09-818-512-3
; Sequence 3, Application US/09818512
; Patent No. 6537780
; GENERAL INFORMATION:
; TITLE OF INVENTION:
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STREET: 333 EARLE OVINGTON
CITY: UNIONDALE
STATE: NY
COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  26.9%;
larity 58.3%;
Conservative
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ilarity 54.5%;
Conservative
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SYSTEM:
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55; Conser
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Query Match
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Best Local S
Matches 55
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FENTION: AMINO ACID MODIFIED POLYPEPTIDES
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US/09/169,76
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1367 GAGCTCAGGGACCCCCTGGCCCTG
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GENERAL INFORMATION:
APPLICANT: GRIFF
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,086
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFREY S.
REGISTRATION NUMBER: 32,063
REGISTRATION INFORMATION:
TELEPHONE: 516-228-8484
TELEFAX: 516-228-8484
TELEFAX: 516-228-8484
TELEFAX: 516-228-8484
TELEFAX: 516-228-8484
TELEFAX: 516-228-8516
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3181 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Pred. No. 7.7;
0; Mismatches
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Patent No. 5821089

GENERAL INFORMATION:

APPLICANT: GRUSKIN, ELLIOTT A.

APPLICANT: GRUSKIN, ELLIOTT A.

APPLICANT: CONNOLLY, KEVIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: DILWORTH & BARRESE

STATE: NY

COUNTRY: US

ZIP: 11553

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
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RESULT 15 US-09-169-768-13 ; Sequence 13, Application US/09169768 ; Patent No. 6492508

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APPLICANT: BUECHTER, DOUGLAS
APPLICANT: BROKAW, JANE
APPLICANT: ZHANG, GUANGHUI
APPLICANT: PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8484
INFORMATION FOR SEQ ID NO: 13:
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1: 3349 base pairs
nucleic acid
EDNESS: single
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FILING DATE:
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MEDIUM TYPE: F1
COMPUTER: IBM F
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10A_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10A_PUB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US10A_PUB.seq:*
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US-10-272-411-4
US-10-272-328A-4
US-10-247-671-68
US-09-932-300-34
US-10-191-997-104
US-10-429-802-33
US-10-430-503-24
US-10-247-671-120
US-10-312-841-1
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	7 7	21	42	0	Н		-10-057-475B-622	equence 622	4
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		4.5	33	Η.			-09-801-371A-10	equence 10,	Appl
	ט	25	31	ω.	S		-10-292-798-14	equence 1463	4
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	U	े चंद्र	27	Ġ	Ý	13	S-10-027-632-88	equence 884	A
		2	27	9	Φ	14	-10-027-632-8	equence 8841	K
		4 3	27	9	89	12	8-10-159456	quence 71,	_
	•	44	27	9	g	13	-10-133-937-7	equence 71,	d
	7	E.	27	9	9	13	-10-354-358-4	equence 43,	ď

ALIGNMENTS

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1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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                                                                                                                                                   EGULATION OF GENE EXPRESSION THROUGH MANIPULATION OF MRNA SPLICING AND IT
                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Osman, Farhat
APPLICANT: Osman, Farhat
APPLICANT: Den-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSI
TITLE OF INVENTION: MANIPULATION OF MRNA SPLIC
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT APPLICATION NUMBER: PCT WO 00/14255
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
5-09-801-371A-1
Sequence 1, Application US/09801371A
Patent No. US20020155569A1
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LENGTH: 104
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Pred. No. 1e-27;
Mismatches
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Pred. No. 1e-
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Ross, F. Patrick
TITLE OF INVENTION: RANKL MIMICS AND USES TH
FILE REFERENCE: 60019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
CURRENT APPLICATION NUMBER: 60/329,393
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILLING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3:1
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LENGTH: 1643
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ X0
DATABASE ENTRY DATE: 1995-03-21
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-05-01
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-05-01
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)..(1643)
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Publication No. US20030100068A1
GENERAL INFORMATION:
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; DATABASE ACCESSION NUMBER: NCBI/
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4
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  Patentin version
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104; Conservative
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                                                                              ; ORGANISM: human
US-10-310-793-9
                    NO 9
TH: 1643
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                SEQ ID NO 9
LENGTH: 16'
TYPE: DNA
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Best Local S
Matches 104
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Best Local S
Matches 104
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SOFTWARE:
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          Sequence 5, Application US/09801371A

Patent No. US20020155569A1

Patent No. US20020155569A1

Patent No. US20020155569A1

APPLICANT: Kaempfer, Raymond

APPLICANT: Osman, Farhat

APPLICANT: Darrous, Nayef

APPLICANT: Ben-Asouli, Yitzhak

TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH

TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES

FILE REFERENCE: A34084-PCT-USA-A 066031.0147

CURRENT APPLICATION NUMBER: US/09/801,371A

CURRENT FILING DATE: 2001-03-07

PRIOR FILING DATE: 1999-09-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 6.3e-28;
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APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Guo-Liang
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Relating To Human Tumor
FILE OF INVENTION: Relating To Human Tumor
FILE REFERENCE: PF573
CURRENT APPLICATION NUMBER: US/10/310,793
CURRENT APPLICATION NUMBER: 60/336,695
PRIOR APPLICATION NUMBER: 60/314,381
PRIOR FILING DATE: 2001-07
PRIOR APPLICATION NUMBER: 60/214,381
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-08
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
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Sequence 9, Application US/10310793
Publication No. US20030198640A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
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Conservative (
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NOS: 71
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104; Conser
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NUMBER OF SEQ II
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Best Local S
Matches 104
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GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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Sequence 1, Application US/09824322B

Sublication No. US20030022848A1

GENERAL INFORMATION:

APPLICANT: Baker, Brenda

APPLICANT: Bennett, C. Frank

APPLICANT: Butler, Madeline M.

APPLICANT: Shanahan, William R.

TITLE OF INVENTION: ALPHA) EXPRESSION

TITLE OF INVENTION: ALPHA) EXPRESSION

FILE REFERENCE: ISPH-0501

CURRENT APPLICATION NUMBER: US 09/313, 932

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 1998-10-05

NUMBER OF SEQ ID NOS: 503

SEQ ID NO 1

LENGTH: 3634
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                              Publication No. US20030194721A1
GENERAL INFORMATION:
APPLICANT: Mikita, Thomas
APPLICANT: Shiffman, Dov
APPLICANT: Shiffman, Dov
APPLICANT: Forter, Gordon, J.
APPLICANT: Raser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CEL
FILE REFERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL Program
SEQ ID NO 68
LENGTH: 1666
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(796..981,1589,.1634,1822..1869,2171..2592)
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Pred. No. 1e-27;
); Mismatches 0;
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                  Application US/10247671
Io. US20030194721A1
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Best Local Similarity 100.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΰ
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyt
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(982)..(1588)
exon
(1589)..(1634)
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ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: 1347, 1358
; OTHER INFORMATION: a
US-10-247-671-68
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NAME/KEY:
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                                                                                                    Treating Metabolic
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Sequence 3, Application US/10218547

Publication No. US20030100074A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Methods And Compositions For Tre;

TITLE OF INVENTION: Human Endokine Alpha

FILE REFERENCE: PF561

CURRENT APPLICATION NUMBER: US/10/218,547

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: 60/312,542

PRIOR FILING DATE: 2001-08-16

PRIOR FILING DATE: 2001-030,761

PRIOR FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                               ; DB 15;
1e-27;
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Pred. No. 1e-27;
Mismatches 0;
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Pred. No. 1e-;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10272328A; Publication No. US20030109444A1; GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES TH
FILE REFERENCE: 60019620-0206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOS: 51
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CURRENT FILING DATE: 2003-01
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity
104; Conser
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: human
                                                                                                                                                                                                                                                                                           ID NO 3
ENGTH: 1643
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TH: 1643
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US-10-247-671-68
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Best Local S
Matches 104
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Best Local S
Matches 104
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RESULT US-10-2

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Sequence 33, Application US/10429802

Sequence 33, Application US/203228285A1

GENERAL INFORMATION:

APPLICANT: HUNG, MIEN-CHIE

APPLICANT: WONG, KA YIN

APPLICANT: WONG, KA YIN

TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER

FILE REFERENCE: UTSC:752US

CURRENT APPLICATION NUMBER: US/10/429,802

CURRENT FILING DATE: 2003-05-05

PRIOR APPLICATION NUMBER: 60/377,672

PRIOR FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 33

LENGTH: 4830
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                                                                                                                                                                APPLICANT: Oligos Etc., Inc.
APPLICANT: DALE, Roderic M. K.
APPLICANT: DALE, Roderic M. K.
APPLICANT: ARROW, Amy
APPLICANT: THOMPSON, Terry
TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological
FILE REFERENCE: 54800-5019
CURRENT APPLICATION NUMBER: US/10/191,997
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,820
PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin version 3.1
         104
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Pred. No. 1.2e-27;
; Mismatches 0;
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1.2e-27;
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Pred. No. 1.2
; Mismatches
                                                                                                                    Sequence 104, Application US/10191997
Publication No. US20030207834A1
GENERAL INFORMATION:
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al Similarity 100.0%;
104; Conservative C
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        GAATCTGGAGACCAGGGAG
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; OTHER INFORMATION: X02910
US-10-191-997-104
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ORGANISM: Homo sapiens
FEATURE:
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; ORGANISM: Homo sapiens
US-10-429-802-33
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Best Local Similarity
Matches 104; Conser
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LENGTH: 3634
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US-10-429-802-33
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Best Local S
Matches 104
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US-09-932-300-34

US-09-932-300-34

Sequence 34, Application US/09932300

Publication No. US20030032788A1

GENERAL INFORMATION:

APPLICANT: GARVER, Eric

APPLICANT: TU, Guang-Chou

APPLICANT: ISRAEL, Yedy

TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION

FILE REFERENCE: 9855-3U2

CURRENT APPLICATION NUMBER: US/09/932,300

CURRENT FILING DATE: 2001-08-20

PRIOR APPLICATION NUMBER: US 60/051,705

PRIOR FILING DATE: 1997-07-03

PRIOR FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 111

SOFTWARE: Patentin Ver. 2.1
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Pred. No. 1.2e-27;
; Mismatches 0;
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Pred. No. 1.2e-27;
Mismatches 0;
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ISSUE: 17

PAGES: 6361-6373

DATE: 1985-09-11

DATABASE ACCESSION NUMBER: X02910 Genbank

DATABASE ENTRY DATE: 1997-02-17

US-09-824-322B-1
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                                                                                                                                                                                                                                                               AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tur
TITLE: chromosomal localization
JOURNAL: Nucleic Acids Res.
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                                                                                                 DUBLICATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Sanith, D.
AUTHORS: Jarrett-Nedwin, J.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: H.m.-
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SOFTWARE: Pater
SEQ ID NO 34
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LOCATION:
NAME/KEY:
LOCATION:
NAME/KEY:
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Patent No. US20020155569A1
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LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                         Patent No. US20020155569A1;
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond;
APPLICANT: Osman, Farhat;
APPLICANT: Jarrous, Nayef;
APPLICANT: Ben-Asouli, Yitzha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 79.2%; 61; Conservative 1
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; LOCATION: (3294164)
US-10-312-841-1
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OTHER INFORMATION:
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LENGTH: 81
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Best Local S
Matches 61
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                                                                            RESULT 12
US-10-430-503-24

Sequence 24, Application US/10430503

Publication No. US20040005684A1

GENERAL INFORMATION:
APPLICANT: LAN, KENG-LI
APPLICANT: LAN, KENG-LI
APPLICANT: LIU, JAW-CHING
APPLICANT: LIU, JAW-CHING
APPLICANT: LAN, KENG-HSIN
TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC
TITLE OF INVENTION: REAGENTS
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APPLICANT: Shiffman, Dov
APPLICANT: Shiffman, Dov
APPLICANT: Raser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REFERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL Program
SEQ ID NO 120
LENGTH: 1279
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GAATCTGGAGCCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC
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Pred. No. 1.2e-27;
Mismatches 0;
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; OTHER INFORMATION: Incyte ID No. US20030194721A1
US-10-247-671-120
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Pred. No. 9.5e-24,
; Mismatches (
                                                                                                                                                                                                                                                                                   FILE REFERENCE: UTSC:797US
CURRENT APPLICATION NUMBER: US/10/430,503
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/383,063
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 4830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 120, Application US/10247671
Publication No. US20030194721A1
GENERAL INFORMATION:
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llarity 99.0%;
Conservative
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Best Local Similarity 100
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-430-503-24
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US-10-247-671-120
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Best Local S
Matches 104
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TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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                                                   GAATCTGGAGACCA-GGGAGCCTTTGGTTCTGGCCAGAATGCTGC
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Pred. No. 3.8e-18
5; Mismatches
                                                                                                                                                                                                                                                                                                                   APPLICANT: Osman, Farhat
APPLICANT: Osman, Farhat
APPLICANT: Jarrous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSI
TITLE OF INVENTION: MANIPULATION OF MRNA SPLIC
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASELSEQ for Windows Version 4.0
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Pred. No.
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